

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCACCAC**CATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCACAGCTTTCCAAAGGCCCTCCCCTGTGTGAAGAATTCATCACGAAGATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACCTGGCCAAAGAACTCAAAGAGGCAGCATTGGAAACCATCGATGGAAAAAATATTTAAAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCCTCAGT
 ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCTCCACTGTGGCCATGTGTGCGCCCAAGTGAAGGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAAATCAAGCGTGCAGAGTAT
 CACCAATGTATGGAGTTCAAANAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATAATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**G**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAATGGGGCAGATATGC
 ATTAATACTGTTGTACAGCAGCTTTCGTTGAAGTTTGAAGATAAGAAACATGTCAATATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAATAAGCACACACATTTTCAATTCATGTTTGAAGTATTTAAAAATGTT
 TTGGTGAATGTGAAAACTAAAGTTTGTGTATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACTAAATTTAGCAAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGAAACAAAGTGGTCATTGTTACATTCATTT
 GCTGAACTTAACAAAACCTGTTCACTCTGAAACAGGCACAGGTGATGCATCTCCTGCTGTG
 CTTCTCAGTGTCTCTTTCCAAATATAGATGTGGTCATGTTTGAAGTTGACAGAAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAACATTCCTCAAGAGAAAATATTCAAAGCATGAAATATGTGCTCTTTTCCAG
 AATACAAACAGTATACTCATG

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRGTQGE
KEAALEPSMEKIFKIDQMGRWFVAGGAAGVGLGALCYGGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMMFMRGWSVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLIGGLLIRAAMYTAGIVGGLSTVAMCAPSEKFLNMGAFL
GVGLGLVFSVSLGSMFLPTTVAGATLYSAAMVGGVLVFSMFLLYDQKVIKRAEVSPLYGV
QKYDPINSMLSIYMDTLNI FMRVATLSTAGGNRKK

FIGURE 3

GAAGGCTGCCTCGTGGTCCGAATTTCGGTGGCGCCACGTCGCGCCGCTCTCCGCTTCTGCAT
CGCGGGCTTCGGCGGGCTTCACCTAGACACCTAACAGTTCGCGGAGCCGGGCGCGCTCGTAGGG
GGTTCGGCACGGGGATCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCTGAAGATGTCGG
ACATTCGGAGACTTGGTTACAGGAGCATCCCGGCGATCACGCGCTATTGGTTCGCGCGCCACCGTC
CCGCTGCCCTTGGTTCGGCAAACTCGGCCCTCATCAGCCCGCTACCTCTTCCCTTCGGCCCGA
AGCCTTCCTTTATCGCTTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
GTCGAGGAACTGGATTTCTTTATTTGGTCAATTTATTTCTTATATCAGTATTTCTACGCGA
CTTGAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
TGTCACTACTTTATGCTCGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGA
ACACGATTTAAGGCCTGCTATTTACCTGGGTATCCTTGGATTCAACTATATCATCGGAGG
CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCCATAATGTTCA
GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
CTGCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC
TGCTGATCAGAATGGCGGAGGCCGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC
AGTGAAGGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCCACAGTGCTGGGTG
CACTTAACAACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
AGTACGAGACAGAGCTTTCTAAATCCCGAAGAAAAATATAAGTGTTCCACAAGTTTCCAGAT
TCTCATTTCAAGTCCCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAAACTGAC
TACATTTTGGTGTCTTCTCTCTCCCTTTCCGTCCTGAATATGAGGTTTACCGGGTCTCT
AATCTGCTGGCATTTGAGCTGGGGCTGGGTACCAAAACCTTCCCAAAAGGACCTTATCTCTT
TCTTGACACATGCCCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
CCATAAAAATTGCTCGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGTC
ACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTGTACCAATAGGGGGGAG
AAGACAGCCACGGATGAAGCGTTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTT
AACCCTTGGCCACTCTTCAGATATTTTTTATAAAAAAAGTACCACCTGAGTTTCATGAGGGCCA
CAGATTGGTTATTAATGAGATACGAGGTTGGTGCTGGGTGTTTGTTCCTGAGCTAAGTGA
TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCAACCC
TTTGCCTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTTGCTTGTGT
TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
ATTCCCATTTCAATCTCATTCTGGATATGTGTTCAATGAGTAAAGGAGGAGAGACCCCTATA
CGCTATTTAAATGTCACTTTTTTGCCTATCCCCCGTTTTTGGTCATGTTTCAATTAATGT
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAAGCACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGAGGTTGTTA
TTTTGAGTCAATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACCTTTTTT
TCGTAGGTGGGCTTTTTCTATCAGAGCTTGGCTCATAAACCAATAAAGTTTTTTGAAGGCCA
TGCTCTTTTACACAGTTATTTTTATTTATGACGTTATCTGAAAGCAGACTGTTTAGGAGCGT
ATTGAGTGGCTGTCACTTTTGGGCAACTAAAAAGGCTTAAACAGTTTTGATCAGTTTCTT
TTCAGGAACATTTGGCTCTTAACAGTATGACTATCTTTCCTCCCACTCTTAAACAGTGTGAT
GTGTGTTATCTAGGAAATGAGAGTTGGCAACAACTCTCATTTTGAATAGAGTTTGTGTG
TACTCTCCATATTTAATTTATATGATAAAATAGTGGGAGAGCTGAACCTTAACTGTCA
TGTTTTGTTGTTTCATCTGTGGCCACAATAAGTTTACTTGTAAAAATTTAGAGGCCATTTACT
CCAATTATGTTGCACGTACACTATTGTACAGGCGTGAGACTCATTTGATGTATGAAGAATA
TTTTCTGACAGTGAGTGAACCGGAGTCTCTGGTGTACCCCTTACCACTGAGCTGCCGCGAG
CAGTCAATTTTTTCTAAAGGTTTACAAGTATTTAGAAGTTTTTCAGTTCAGGGCCAAATGTTT
ATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTTGATTTTGTCTGGATT
ATGTTTCTGGAATAATTTTACCAAAACAGCTATTTGAGTTTGTACTTGACAAAGGCAAAACA
TGACAGTGGATTCTCTTTTACAAATGAAAAAATAATCTTATTTGTATTAAGGACCTTCC
TTTTTGTAAACTAATCTTTTTTATTTGTAATAAATGTAAATTAATGTCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGKISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCGTTGCC
 CCTTGGGGCGGG**ATGG**CTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGAGAGCATCG
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGTTACCTCAAAGAAATGGAAAT
 AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAGGAAAA
 AACAGTTATCAGAGGCTAAACAGAAAGGCCACAGTGCAATTCAGTGAAGCTGCAATAATG
 AATAATCCCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGAAAGGTTCTGAACTTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTAGTC
 CTTACACTG

MAAEEDDEVEVWVESIAGFLRGPDWSIPILDVFEQKCEVNCKGGHVITPGSPFEPVILVACVP
LVFDDEEESKLTYTEIHQYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAEDFTTFKAMMVQKNIEMQLQAIRIIQERNVLPDCLTDGSDVVSDDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSAEAIMNNSQGDGEHFAHPSEVKMHFANQS
IEPLGRKVERSETSSLPGKGLKIPGLEHASIEGPANLSVLGTETELQRHLYLKQKRDKLMS
MRKDMRTQKIQNMEEQKGKPTGEVEEMTEKEMTAEESEKQTLTKRRLAEKLEKEEVIN

amino acids 224-228, 246-250, 285-289

amino acids 273-279

amino acids 252-256

amino acids 78-108

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAGCTGTTAGAAGTTACTCCTAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTGCAAGACCCATACATCACAG
GCCATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAACATGTAATGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTA
CTGACTGCTTACCAGTGGCTGATGTGGTCTGAGTGACCTTGGAACCGAAGAGATGAAAT
CCTGAGGGGAAGTCTTAGAAATCAAAGAGGAATGATGACCAGGAA

CGGTGGTTTTTGTCTTCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCATACCTACTG
TAGCTTCTCCAGCATGAGCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTACTG
TCTCAGCTTCAGATGTCGCGTTCTTCCACTAGAAGCTCTTCTGAGGAGGTAATTAAAAAAC
AGTGGAAATGGAAGAAACAGTGTCTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC
ATTCCTGCTGATGTCCTCATATGCTTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
TGCCAAATGAAGAAACAAAGTATGATATCTTCCAACACTGCTGAATGTGTCTCAGAAGCTG
GTGAAGCTAGTTTTCTGTGTCTTGTGTCACTTGTGTTATATAAGAAAGATCATCAAAAGTAG
AAATTTGAAATATGCTTCTGGAAGGAATTTCTGTGATTCATGAAGTGGTCCATCTCGCT
TCTTTATTTCTCGGATAACTTGATGTCTCTATGTCTGCTATPCTTCAACAGCACTG
GCTGTATCTTCTCAAAATTTAGCATATTAACAACAGCTCTTCTATTCAGATAGTGTCTGAA
GAGGCGCTCAAACCTGGATCCAGTGGGCTTCCCTGACTTTTTTTTTGTTCTATTGTGGCT
TGACTGCGGGGATAAAAATTTACAGCACAACTTGGCAGGACGTGGATTTCATCAGGATGCC
TTTTTCAGCCCTTCCAATCTGCTGCTCTTTTCAAGAAGTGAGTGTCCGACCAAGAACATTTG
TACAGCAAAAGGAATGGACTTTTCTTGAAGCTAAATGGAACACCAAGCAGAGATTTTCAGTC
ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTATTTCITCAATGGCT
AATATCTATAATGAAGAAGTACTGAAGGAGGGGAACGCTCACTGAAGACATCTTCATACAGA
GAACAGCAAATCTGATTTCTTTGGCATCTGTTTTTAATGGGCTGACTCTGGGCCTTCAGAGA
GTAACCGTGATCAGATTAGAAGATGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
CTTATTTTTGTAATGTCATTCAGGGCCCTTTCAGTGGCTTTTCATCTGAAGTTCCTGGATA
CATGTTCCATGCTTGTATGGCCAGGTACCACGTGCATTATCAACAAGTGTCTGTCTGG
TCTTTGACTTTCAGGCCCTCCTCGAATTTTTTCTTGAAGCCCATCAGTCTCTCTCTATA
TTTTATTATAATGCCAGCAAGCTCAAGTTCCGGAATACGCCATGAGCAAGAAAGGATCCG
AGATCTAAGTGGCACTTTTGGGAGCGTTCCAGTGGGGATGAGAGAAGAACTAGAAGACTTA
CCAAACCCAGAGTGTAGTGATCAGATGAAGATACCTTTCAACTGGTACCACATAGTTTGA
GCTCTCTTGAACCTATTTTTTCACATTTTTCAGTGTTTGTAATTTATCTTTTTCATCTGATA
AACCAGAAATGTTTCTAAATCCTAATATTCTTGCATATATCTAGCTACTCCCTAAGTGGTT
CCATCCAGGCTGTAGAGTACCCAAAGGCTAAGAATTTCAAAGAACTGATACAGGAGTAACA
ATATGAAGAATTCATTAATATCTCAGTACTTGATTAATCAAAGAGTTATATGTGTCAGATTAT
TTTTCTTGGCCTTCAAGCTTCCAAAACCTTGTAATAATCATGTAGTCTAGCTTGTAAT
ACACATAGAGATCAATTTGCCAAATTTACAACATCATGTAGTCTAGTTTACATGCCAAAGT
CTTCCCTTTTAAACATTATAAAGCTAGGTTGTCTTGAATTTTGGGCCCTAGAGATAGT
CATTTTGCAGTAGAAGAGCAACGGGACCTTTTCTAAAACGCTGGTTGAAGGAGCAATAATAC
CTGGCCATACCATAGATTTGGGATGTAGTCTGTGCTTAAATTTTGTCTGAAGAACGAGT
TTCTCAGACACAACTCATCAGAATTTTAATTTTAGAATTCATGGGAAATTGGATTTTTGT
AATAATCTTTTGTGATTGTTTAAACATTTGGTTCCTTAGTCCACATAGTTACCACCTGTGATTTTA
AGTCATTTAAACAGGACCGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAACTCTGAT
GTCATTACTCTGAATTATTCATTTTGGAGAATAAGAGGGCATTTTTATTTTATTAGTTACT
AATTCAAGCTGTGACTATTGATATCTTTCCAAGAGTTGAATGCTGGCTTCAGAACTCATAC
CAGATTGTCAGTGAAGCTGATGCTTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
AGCAAACACATGTGACTTTTAACTGATGTATGAATATTAATCATCTTAAAAATAGAAGAC
AGTAATATATAAGTCACCTTTACAGTGCTACTTCACACTTAAAGTGCAATGGTATTTTCATG
GTGATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATTTAA
AAATTAGCAACCAAAAGTACATTTGCTCAGGGTCACTGACGCTGGGTGATGATAGAAGAGTGG
CTTTAACTGCGAGCGCTGATGTTTTCAGACATACATATGTAATATGAGCTTTATGCTTTGTGTT
CATTTCTCAGAAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
AGGTAATATACATATATAATTAATTCATTTGTGATATCCACAATAATATGACTGGCAGAAATTTG
GTGGAAATTTGTAAATTAATTAATTAATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSASFVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESEDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAACAGTGGAAATGGAA
AAACAGTGTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAAC TACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCCTGATTT CATGAAGTGGTCCATTCCCTGCCTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATT CAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGGCGGC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGCGAGAGGAGCAT
 CCCGCTCTACAGGTCCTCAAGCGGCGTGGCCCGCGGGTCTATGGCCAAGGAGAAGCGCCGAG
 AGCGGCTCCGCGGGCGGGGCTGCTACCCACAGCATCCTCCAAAGCACTGAACGCCCGGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACAGGTGACGGGCTGTGCCCTGGTTCCTTCCCTCAGATCTAC
 CTATTGCATGTGGCTCAGGTGGGCCCCCTTCTCTGCCCTCCATCATCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCTCTGCATCAGCAAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCCGCTATTGCCCTACTTCCCT
 ATCTGGTTCGTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATTGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCTTGTTCACAG
 ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACCATACATGGCACCCTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCACTGTCTGTATCTATATAATCTG
 TGCTGTCTCCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAATTT
 ATTACTGGCTTCTCTTACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGCTCTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATTCCCATCTGGCAGTGGTTCCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCGTGTATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGCTTCTTCCACCAAGTTTGCCTCTGGAGTGTG
 ACTGGGCATTTCTACCCTCAGTCTGGACTTTGACGGGTACAGACCCGCTGGCTGCTCGCAGC
 CGGAACGCTGTAAGTTTACACTGAACATGCTCGTGACCATTGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGGCGGAGAAAGAA
 GGCCTTGACGGCACTGAGGACGAGGCCAGCAGCTTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTCTAGGGCCCCGCCACGTTGCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGCTTGTGACGAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCTGTGCTCACTGTGGGCGGGCTGCTCTG
 TGGCCTCTGCTCCCTCTGCTGCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGTAATA
 TGCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

MWLRWALS L P S S C L W A E P G M P S Q T P W W A S A N P P G P A W V A L C P G S S S P R F W P S L P T S S S G
S C P T S H T A R P I G T C F S I A S L K Q W S R V S M F P T R L S P C S S A T E Q T E R D S A T A Y R M T E V L G T V L
G T A I Q Q Q V I G Q A D T P C F Q D F N S S T V A S Q S A N H T H G T T S H R E T Q K A Y L L A A G V I V C I Y I I C A V
I L I G V R E Q R E P Y E A Q Q S E P I A Y F R G L R L V M S H G P Y I K L I T G F L F T S L A F M L V E G N F V L F C T
Y T L G F R N E F Q N L L A I M L S A T L T I P I W Q W L T R F G K K T A V Y V G I S S A V P F L I L V A L M E S N L I
I T Y A V A V A A G I S V A A F L L P W S M L P D V I D D F H L K Q P H F H G T E P I F F S F Y V F T K F A S G V S L G
I S T L S L D F A G Y Q T R C S Q P E R V K F T L N M L V T M A P I V L I L L G L L L F K M Y P I D E E R R R Q N K K A L
Q A L R D E A S S S G C S E T A S F A S I L

FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCCTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

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FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATG
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTTATGTTCTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTCTGGAATACTGAGTTGTTTAGG
ACTTCTATTTGTGGCAAACCTCCAGAAAAACAACCCCTTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTTCAGACCATCCTTTCCTACCAAATG
CAGCCCAAAATCCATGGCAACAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
ATTTAGAAACAGAAATCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGAAAGGTTACAGAAGTTGCTTA
TTCCTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

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CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAAATCAGCGTCTAATTAAATCCTCTGGTTGTGAAGCAGT
TACCAAGAATCTTCAACCCCTTCCCAAAAAAGCTAATTGAGTACACGTTCTCTGTTGAGTACA
CGTTCTCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAAACAAAAACCTGTTAGAAAATGTGGTGGTTTTCAGCAGAGCCCTCAGTTTCCCTCCT
TTCAGCCCTTGTAATTTGGACATCTGCTGCTTCATATTTTCATACATTACTGCGAGTAACACT
CCACCATATAGACCCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTTCGCCGGCTGCAC
 CTTGCTTGTACTTGTCTGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGCGAGAGCTGCGGAGCTCTCTGAG
 GTCTTCGAGAGTACCGGAAGGAGCACCAGGCCCTACGTGTTCTGTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAAATTTCTCTGTGT
 GCAGACAGGGTCCATCTGTCAACCTAACCTCTCTGGATGCTTTTTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGATGACTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGAATGGA
 TGTGGTCCTCTAAAGCCCCCTCATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCTAGAAAATGCTGTTGT
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 AAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
KEHQAYVFLFCGAYLYKQGFAPGSSFLNVLGALFGPWLGLLLCCVLTSVGATCCYLLSS
IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCGCATGAATCATTTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACGCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATCGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAAATGAACCTCAGAGACC
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTTCAGCCATTAGCACCTGAGCCAGTGTCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGTCATGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCGC
 AACTGCACTGGCTGTGCCGAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCAACCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTATCATTTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTG
 ACACCACCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCTATCTGCGAT
 GGAACCGCTTTCTCAGAAGTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAAA

MDLAANEISIDYDKLSETVDLVRQTGHQCGMSEKAIEKFIQRLLEKNEPQRPPFPQYPLLIIVVY
KVLA TLGLILLTAYFVQIPFSPLAEPVLSGAHTWRSLIHHIRLMSLP IAKYMSENKGVPL
HGGDEDRFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFAKWWRCFPERWFFPPYPWRRPLNRSQMLRELFPV
ETHLFPVDDASLNKCSFLHPEFVSGSKMKHMPDLFI IGSGEAMLQIIPFQCRRHCSQVAMP
IEPGDIGVDTTHKWVYIARGVQPLVICMDGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATAGGAAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAAGAAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQAQTHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALET
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPSPQGYLSSRPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSDRQFHSVAAAWQARLESPADVKEIIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDDVLPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIIFYGKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSEAAEAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPTMGSHKTQRLLSGFPWPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLSIGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSA
 WERPGAQVTVSYLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGLKLI VVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC
 TGGACCCCTTAAGTGGGTACTGGCCCTGGGCCAATGCGTCCTCGTGGAGCCTTTGCCCTCCTT
 CTACTGGGCCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTCTCTGGACAAAATGCAGAA
 CCTGCTGTCTGTTCTTTGGGAAGCTGCTGGTGGTTCGGAGGCGTGGGGTCTCTGTCTTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT
 TTTGGGCATGTGTGTGGACACGCTCTTCCTTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC
 ACCCACCCCCACCGTCCAGCCATCCAACCTCACITTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAATAAATAAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGTTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTCGTGTCGCGATTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATCTTCAACCTGATGAAGACACTATATTCTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGGCAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACAACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 CGGCTCCAGGAGTTCCTTGCAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTGTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACAGCTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTGGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAATCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATGGCAGCTGC
 CTTTGCACCAACCTCGTCATCTCCAGGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAACACCTGCTCA
 AGTCCTTTGTGTGTTGACAAAGAACCAGCGCTGCAAACTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAAGAGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCCTAGGAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAACCTGGCTTTCATTAGATTGTAAGTTATGGACATGATTGAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDDETIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDEEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLCNTSYTAARFKLWSVHGQKR
LQEFLLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGI PPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTCCAGTGTGACCANGTGCAATATANGCT
GGTTCCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAAGTGTGGAGCTAATGTAGACCTATTGGATATTCTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

[illegible]

FIGURE 30

MVTAALGFPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDGPGMGLPGYMGREGPQGEFPGQSGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117



FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGACCGCCAGGAAAGACTG
 AGGCGCGGGCTGCCCGCGCCGGCTCCTGCGCGCGCGCGCTCCCGGGACAGAAAGTGTG
 CTCACAGGGTCCCTCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGACAGG
 GCTGCCCATCCGGCTGCCAGTGACGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCCTTTGAGAACCGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCTGCCGGCTCGAGCTCCTGGACCTGTAC
 AGAACCCAGATGCCAGAGCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAAATCACCAGTGAGACCTTCCGTGGCTGCGCGCCCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCTTCGACACGC
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTACGCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTGCGGTGGCCGGCAACAC
 CCGCATTTGCCAGCTGCGGGCCGAGGACCTGCGCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCTTGCAGGCGCTGCCCTGGCGACCTCTCGGGCTCTTCCCGCGCTGCGG
 CTGTGTCGAGCTGCCCGCAACCCCTTCAACTGCGGTGTCGCCCTGACTGGTGTGGCCCGCTG
 GGTGCGGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACC
 ACCACAGCCACAGTGCCCAACCCAGAGGCGCTGGTGCGGGAGGCCACAGCCTTGCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGCTCACCTGCTC
 AATGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCA
 CGCCGAGGCCACCACGCTCCCTGACCTGGGCATCGAGCGGTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTCAACCAGCTGCGGCCCAACGCCACTTACTCCGCTGTGTGTCATGCCCTTGGGG
 CCCGGCGGGTGCCCGAGGGCGAGGAGGCTGCGGGGAGGCCCATACCCCCAGGCTGCCA
 CTCCAACACGCCCCAGTCACCCAGGCCCGCGAGGGCAACCTGCCCTCCTCATTTGCGCGCG
 CCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGG
 GGGCGGGCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC
 GGAACGTGAGGGAGTGAAGGTCCCTTGGAGCCAGGCCCAAGGCCAACAGAGGGCGGTGGAG
 AGGCCTGCCAGCGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTCGGCTC
 CAGTCACCCCTCCACGCAAGCCCTACATCTAAGGCCAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCAAGTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGGCTGTTCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGCCCTGCCATGTCTGGTAACGCATGCTGGGTCTGCTGGGCTCTCCACTCCAGGGCGGA
 CCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGCAGAGGGAGAGCGGTTAGCGCGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATTTATAAGAGATCCTTCCATTTATTCTG
 GGAAGATGTTTTTCAACTCAGAGACAAGGACTTTGGTTTTTGAAGACAACAGATGATATG
 AAGGCCCTTTGTGAAGAAAAATAAAGATGAAGTGTGA

FIGURE 32

MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVFEN
 GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
 RLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
 GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG
 NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVPLSWFG
 PWVRESHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALS
 SSLAPTWLSPTAPATEAPSPPTAPPTVGPVPPQDCPPSTCLNGGTCHLGRHHLACLCPE
 GFTGLYCESQMGQGRPSPTPVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQSSSVQLRSLRL
 TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA
 VHSNHAPVTQAREGNPLLIAPALAAVLLAALAAGVAAVCVRRGRAMAAAAQDKGQVGPAGAG
 PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCGAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAAACTCCTTGAAAAATACAATGAGAGCTCATCAG
 AACCATTTACATATTTTGATGATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAAGCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGAGCTTG
 ACCCGAGCCCAACACGACACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA
 TTTTCTATCTCTGCTCAAACCTGAGAGTTTGTATTCTATGCCATAACAGAATTCACACAGCTGG
 ATCTCAAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGTCCTCAGGTATTTAGATCTTTCTTTTAAAGACTT
 TGACACCATGCCATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAAACAAAAATCAGATTTCCAGAAAAATTGCTCATCTGCATCTAAATCTGTC
 TTCTTAGGATTCAGAACTCTTCTCATTTATGAAGAAGGTAGCCTGCCATCTTAAACACAAC
 AAACTGCACATTTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAAATATTAGAAATGACAAATATAGATTGGCAAAAGCCCAATTTGTAAGTATGAA
 ATGCAACGAAATCTTAGTTTTAGAAAAATGCTAAGACATCGGTTCTATGTCTAAATAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAAATTTGTTTGGCATACATCAGTGGAAACACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTAC
 TCAAAATCTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTCAGAGTGTTTTACATTC
 ACAGAGTAAAACTTATTTGCTTTTGACCAAAATGGACATAGAAAACTGACAATTTCAATG
 CACAAATGGACACACTGCTTTTCCCGAATTATCCTACGAAATTCCAATTTTAAATTTTGGC
 AATTAATATCTTTACAGACAGAGTTGTTTAAAAGAACTATCCAATCGCTCACTTGAAAACTCT
 CATTTTGAATGGCAATAAATCTGGAGACACTTCTTTAGTAAGTTGCTTTGCTAACACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAATTTGCTCA
 TGGCCAGAACTGTGGTCAATATGAATCTGTATACAATAAAATTTGTCTGATTCTGTCTCAG
 GTGCTTGCCCAAAAGTATTCAAAATCTTGACCTAAATATAACCAAAATCCAAACTGTACCTTA
 AAGAGACTATTCTCATGTGCTGATGCCCTTACGAGAACTAAATATTTGCAATTTTCTAAGTGT
 CTCCTTGATCGAGTCATTTTCAGTAGACTTTTCAGTTCTGAACATGAAATGAACTCTATCT
 CAGCCCATCTCTGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTTAATGCGGGGAAGAA
 ATCCATTTCCGGTGTACCTGTGAATTAATAAAATTTTCATTCAGCTTGAAACATATTGAGAGGT
 ATGATGGTGGATGGTCAGATTATACACCTGTGAATACCCTTTAAACCTAAGGGGAACATAG
 GTTAAAGACGTTTCTCTCCACGAATTAATCTTGCAACACAGCTCTGTTGATTGTACACATTG
 TGGTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGGCC
 TGGTATCTCAGGATGCTAGGTCATGACACAAACATGGCACAGGGTTAGGAAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCAATTTATTTATACAGAGTGAACATGATTTCT
 TGTGGTGAAGAAATGAATGTATCCCCAATCTAGAGAAGGAAGTGGTTCTATCTTGTATTGCT
 CTTTATGAAAGACTCTTTGCCCAACCAATCTCTTCCATGAAAAATTCGATCATATAATTTCTATC
 TTACTGGAACCCATTCATTTCTATTGCAATCCCCACAGGTATCATAACTGAAAGCTCTCTCT
 GGAIAAAAAAGCATACTGGAAATGGCCCAAGGATAGGCGTAAATGTGGGGCTTTCTGGGCAA
 ACCTTCGAGCTGCTATTAATGTTAATGTATAGGCCACAGAGAAATGTATGAATCGCAGACA
 TTACAGAGATTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCATGAGAACAGAGTTGTCT
 ATAAATCCCACAGTCTTTGGGAAGTTGGGGACCATACATGTTGGGATGTACATTTGATA
 CAACCTTTATGATGCCAATTTGACAAATTTTATAAAATAAAAAATGGTTATTCCTCTCATA
 TCAAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAACACCTTCACAAAGTTTATPAAG
 GCTTATGGAAAAAGGTGTTCTCATCCAGGATTTGTTTATAATCATGAAAAATGTGGCCAGGTGC
 AGTGGCTCACTCTGTAATCCCAGCAGCTATGGGAGGCCAAGGTGGGGTGGCCACAGGATCAA
 GAGATGAGAGACCATCTGCCAACATGGTGAACCTGTCTACTAAAAATACAAAAATCA
 GCTGGGCGTGTATGGTGCACGCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCAGGAGATCG
 CTTGAAACCCGGAGGTGGCAGTTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCAATGGCCACAAAAATAGGCTCAATTCATAAAATTTATAGTACATTAATGTAATATAATATTA
 CATGCCATCAAAAAAATAGGAGTGTATATTTTCTGGTATGAAAAAATCAATTAATAT
 GTTATAAACTATTAGGTGGTGGTGCACAACTAATTTGGGTTTGGCCATTGAAATGGCATGAA
 ATAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTGGGAGGTTTGA
 TTACAGGAGCATTTGATTTCTATGTTGTGATTTCTATAATGTTGAAATGTTTGAATATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTCACAGCTT

FIGURE 34

MRLIRNIYIFCSIIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTATTTLDSLNNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDFNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILTDELfKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLQHKNDENCsWPETVvNMNLSYNKLS
DSVFRCLPKSIQILDlnnnQIQTVPKETIHLMALRELNIafNfLTDLPgCSHFfSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFcCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYfDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEwCHYEFYfAHNHLFHENSdHILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTfTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTTCTGGGCTTGGCTGCTTGAACACCTGCCTCCAAGGACCGGCTCGGAGGGGTGCCGGGAAAGG
 GAGGGAAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCGCCCGCGCCTCTGCGCGCCCTGTGCCGCCGGGCG
 CCAGCCGAGCCCGGCGGGCGGGCGGGTACACGCGCGAGCCAGCGCGCGCTCCGCGCGCCCAAGCGCGCCGCT
 CTGCTGTGCCCTTGCCCTTGCCCCGCGCCAGCTTCTGCGCCGCGAGCCCGCGCGCGCCCGGTCACCGTGGA
 CCTGCTCCTGGGCGCGGGCGGAGCAGGCA**ATG**TCCCGCCCGGGGACCGCTACCCAGCCGTGCCCTGTGGTCTC
 CTGGACGTGACCCCTGGCCGGGTGCGAGCCAGGGCGAGCCCTCGAGGACCTGATTATTACGGGCGAGGATGT
 CTGGAGCCGGGAGCCCTACTACGCGCGCCGGAGCCGAGCTCGAGACCTTCTCTCCGCGCTGCTCTGCGGGGCG
 CGGGGAGGAGTGGAGCGGCGCCCGCAGGAGCCGAGGCCCGCCCAAGAGGGCCACCAAGCCCAAGAAGCTCCC
 AAGAGGGGAAGTCCGCTCCGAGCGCGCTCCACAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAG
 CTCTGAGAAGCTGCCAAGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGAGTTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGACTCCAGCTCCATGCCCTCCAGCTGAAGCGCTATGGCTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTATGAAATGATTTTTATGACGGAGCGTGGTGGCGGGGAAG
 AATAGACTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCTGACCAGATTCACTGGTGTCTCACTCAAGGGA
 GGAACCTCCCTCGGTGAGTGACTGGGTGACATCCTATAAGGTCACTGGTGAGCAATGACAGCCACAGTGGCTC
 ACTGTTAAGAAATGGATCTGGAGACATGATATTTAGGGAAACAGTGAAGAGGAGTCCCTGTTCTCAATGAGCT
 ACCCGTCCCATGTGTGGCCGCTACATCCGCATAAAACCTCAGTCTGGTTTATGATGAGGAGCATCTGCATGA
 GAATGGAGATCCTGGGCTGCCACTGCCAGTCCCTAATAATTTATCACCCCGGGAAGCGAGATGACCACTCT
 GATGACCTGGATTGAGCACCAATTAAGGAAATGGCGAGTTGATGAAAGTTGTAATGAAATGTGTTC
 CAATATCACAGAAATTTACACATTTAGAAAAAGCCACAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATC
 ACCCTGGGAGCATGAAGTCGGTGGCCGAGTTCCACTATCGCGGGGCGCCAGCGGCAATGAGGTGCTGTGGCG
 CGGGAGCTGCTGCTGCTGCTGGTGCAGTTCTGTGTGAGGAGTACTGGCCGGAATCGCGCGATCGTCCACT
 GGTGAGGAGACGCGGAGATTCACTGCTCCCTCCCTCAACCCCGACTGACGAGAGGCTACGAAGAGGGGCT
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGAGCCACGATGGAATTGACATCAACAACAACTTTCCTGATTTA
 AACACGCTGCTCTGGGAGGACAGGAGATCGACAGAAATGTCCCAGGAAAGTTCCCACTCTATTGCAATCCC
 TGAGTGGTTCTCTCGGAAATGCCACGCTGGCTGCCGAGACAGAGCAGTCTAGCCTGGATGGAAAAATCCC
 TTTTGTGCTGGGCGCAACTCGAGGGCGCGGAGCTGGTGGTGGCTATCCCTACGACCTGGTGGCTCCCCC
 TGGAGAGCAGCAGGAACACACCCCAACCCCGATGACCACTGTTCCGCTGGCTGGCCTACTCCTATGCTCCAC
 ACACCGCTCATGACAGACGCGCGGAGGAGGTGTGCCACAGGAGGACTCCAGAGGAGGAGGGCACTGTCA
 ATGGGCTCTCTGGCAACCGTCTGCTGGAAGTCTGAACGATTTCACTACCTTATACAACTGCTTCGAACATG
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGAGAATAACCGGGAATC
 TCTGATCGTGGTTATGGAGCAGGTTTATCGTGGCATTAAAGGCTTGTGAGAGATTACATGGAAGAAATCC
 CAACGCCATTATCTCCGTAGAAGGCATTAAACCATGACATCCGAACAGCCAAAGATGGGATTAATGCGCCTC
 CTGAACCTTGAGAGTATGTGGTCAAGCAAGGCCGAGGTTTCACTGCATCCACAAGAACTGTATGGTTGG
 CTATGACATGGGGGCCAAGGTGTGACTTCACTTACCAATAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGG
 AGAAGTTTGGGAGACGCGCTGAGCTGCGAGCCAGGCGGTGAAGCTGCGGGGGCGGAAGAGACGACAGCGT
 GGG**GA**CGCCCTCTGGGCGCTGAGACTGCTGCGGACCCATGCAAAATTAACCAACCTGGTAGTAGTCCATAG
 TGAGACTCACTCACTGTGGTTTCTCTGTAATTAAGAAGTGCTGGAAGAGAGGGTGCAATTGTGAGCAGGTCC
 CAAAGGGAAGGCTGGAGCGTAGGCTGTTCTTTCTTTGTTCCCAATTGATCCAAATTAAGTTGGGACAGAGCA
 GCAGAGAAAGCTGATGGGAGTGAGAGAACTCAGCAAGCCAACTGGGAATTCAGAGAGAGAGAGAGAGGAGG
 GAGCCTGTCTGCTCAGAGCCTCGCTGCTAGAAAAGGATCTCTGGTCTCTCCCTGTTTGGCTGGCGAGCAAGG
 GTTCCACGTGCATTGCAAAATGGCAAGCTAAAATTCAGCACTTCCCCAGCTGGGCTGTCCAAATGTATTTAC
 TTTGAGATGCTCCAGGCGCTCTAAGAGAAATCCACCTCTCTGGCCCTGGGACATTCGAAGTGTCTCAAAATTA
 ATTCTGTGTTCTTTGACAAATGGCTCATTGCCAAGTGCACATCAGTGAGCCTCTGAAATCTGTTTGTCTCTCT
 TTTTCAACAAAGAGTGTGTTTCAGAAAAGGAGAGAGGCTGAGATCACTCAGGAGTTTGTGTGGGACAGACGA
 TGAGCTCTCTTGACAAATCTTGGGTCCTAAGCAACCCCAAGTCCCTGCTGATCCAGTCCAGTCCGCTGGAGTT
 CCCCAGGTAGGAGAGGCGAGAGGTGGCAGCCTTCTGAGGGGCGAGAAATTTAGCCTGGATTCCTCTTTTAC
 CTCTAGGACTGGAAGAGCGGAGGATGGGTGGCTGAGGCGCTCTCTGCTGTGAGGTATTGCCCTGTGTG
 GAATTGAGTGTCTATGGGTTGGCCTCATACAGCTGGGAGTATTTTGTATGTGAAATGCCAGATCTTCCA
 GATTAGGCTAAATGTAATGAAACCTCTTAGGATTCTGTGGAGGAGATCTGGGAGAGAAATTTGAAATTA
 CTTTGAAGAAAAGATATGCTCACTTTTGTAAATGTGCTGCTCATTGACCTGGGAAAAATGAAAAAAA
 AATAAAGCAATGGTAAGACCTTTAAAAAAAATAAAAAAAAATAAAAAAAAATAAAAAAAAATAAAAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYQGQEIWSREPPYARPEPELETFSPPPLP
AGPGEEWERRRPQEPREPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPLPLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
TDDLDFKHHNYKEMQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGWSLGRWTHDGI DINNNFPDLNTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGKGLVRDSHGKGINPAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKEGFTASTKNCMVG YDMGATRCDFTL SKTNMARI REIMEKFGKQPVSLPARR
LKLGRKRQRG

FIGURE 37

CTAAGAGGACAACATGAGGCCGCGGCTCTCATTCTCTAGCCCTCTGTCTCTCTTGGCCAAAGCTGCAGGGG
 ATTTTGGGGGATGTGGGACCTCCCAATTCCCAGCCCCGGCTTCAGCTCTTTCCAGGTGTGTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCCAATGTTT
 TTCCAATTTCCAGCGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTCCTGCCAGACACCACCTTTCC
 CCGTGGACAGAGTGGAAACCTTGGAAATTCACAGCTCATGTCTTTCTCAGAAAGTTTGAGAAAGAACTTTCTAAA
 GTGAGGGAATATGTCCAATTAATAGTGTGTATGAAAGAAACTGTTAAACCTTAAGTGTCCGAATTGACATCAT
 GGAGAAGGATACCATTTCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCTACACCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTGACCAGCTGGAGGTGGAGATAGAATAAT
 ATGACTCTCTTGGTAGAGAGCTTGAGACACTAGACAAAAACAATGTCTTGGCAATTCGCGGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAAACACCCCTGTGCTCCACCCCTCTCCCACTC
 CAGGGAGCTGTGGTCAATGTGTGTGCTGAACATCAGCAAAACCGTCTCTGGTTACAGCTCAACTGGAGAGGTTT
 TCTTATCTATATGTGCTCTGGGGTAGGGATTACTCTCCCAAGCATCCAAACAAAGACTGTATTGGTGGCGGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGTCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGCCCAAGGTAGTGGTAGCAGAGTTTACAACAACACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTTGACCACCAACACGATTGTCTGTGACTCAAACTCTCCCTAA
 TGCTGCCCTATAATAACCGCTTTTATATGCTAATGTTGCTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTTCATGGTATGTGGGGTTCT
 GTATGCCACCCGTACTATGAACACCAGAACAGAGAGATTTTACTATATGACACAAACACAGGGAAGAGGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTCAGAGCATTTAACTATAACCTTTTGGACGAAA
 CTTTATGTCTATAACGATGTTACCTCTGTAATATGATCTTTCTGTCTTGCAGAAAGCCCGCTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAATAGTCTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAAGTGTGTCTATTTTGCAGCAATGTTTAGGTGCATAGTCTTACCACACTAGAGATCTAGGACATTTGTCT
 TGATTGGTGAGTCTCTTGGGAATCATCTGCCCTCTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGA
 TTGTGAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTCTACTAGAAGCCCTTAAATTA
 GGAATTAAGGAACCTAAAACTCAGTATGCGCTCTAGGGATTCTTGTACAGGAAATATTGCCAATGACTAGTCT
 CTCATCCATGTAGCACCACATAATCTTCCATGCCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT
 GGAAGCTCCTCGAGGGACCAATCTCCAACTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAGTGCTGAGTTTTATGGAGAGAGGCTTTTT
 ATGCATTAATTTGTACATGGCAATAAATCCAGAGGATCTGTAGATGAGGCACTGCTTTTTCTTTCTCTC
 ATTGTCCACTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCTTCCAAAGGCAGCTCAGAAGATTAG
 AACCAGACTTACTAACCAATTCACCCCCCACCACCCCTTCTACTGCCTACTTTAAAAAATTAATAGTTTT
 CTATGGAACCTGATCTAAGATTGAAAAAATTAATTTCTTTAATTTTATTATGGAATTTTATTACATGACTCTA
 AGACTATAAGAAATCTGATGGCAGTGAACAGTGAACAGTATGAGATTTATGTTATCTAATAAAGACCTGGAGCAT
 TCTGCAACTCTATGAGTGTATCAGTGTGTCATGTAAATTTTGCCTTTGTTAAGCTCGGAACCTGTAAGAAAT
 GAAATTTTAAATTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTCTAGTTAATCAGTCACTAGT
 TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTGATGACTTTATCACTAGTCTTTGTCTATT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTTACTCCCCCTTTTAAATAAATGAT
 TAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAA

MRPGLSFLALLFFLGLQAAAGDLGDVGPPIPSPGFSSFPFVDSSSSFSSSSRSGSSSSRSLGS
GGSVSQLFNSFTGSGVDDRGTCCQCSVSLPDTTFFPDRVERLEFTAHLVSQKFEKELSKVREYV
QLISVYEKKLLNLTVRDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSQPHPNKGLYWVAPLNTDGRLLLEYRYLNTLD
DLLLYINARELRITYQGSGTAVYNNNMVYNNMYNTGNIARVNLTTNTIAVTQTLPNAAYNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MCGVLYATRMNTREELIFYYDNTNGKEGKLDIVMHMKQEKVQSYINYNPFDQKLYVYNDG
VLLNYDLSVLOKPO

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAAACACCCCTGTCGTCCAC
CCTCTCCCACCTCCAGGGAGTGTGGTCATGGTGGTGTGGTGAAACATCAGCAAACCGTCTGT
GGTTCAGTCTAACTGGAGAGGGTTTTCTTATCTATATGGTGTGGGGTAGGGATTACTCTC
CCCAGCATCCAACAAAGGNATGTATTGGNGGCCCATTTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTCAACCCCATGGATGATTGCTATTGTATATAAATGCTCGAGAGTT
CGGGATCACCTATGGCCAGGTAGTGGTACAGCAGCTTCAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACTGACC

CTCCGACATAGTAAATATCTCGGAAGAAGCGGAAAGAAGCTGTCTCCATCTTGTCTGTAT
CCGCTGCTCTTGTGACGTTGTGGGAATGGGGAGCGCTCGGGGCTGTGCTCCAGGCGAGCT
GGATACCAATGTTTGTGTGGAAGTGGCCCGTGTTTGCATATGCCGATGCTGCTCTAGTGGAAAC
AATCCCACTGTAACTAGATGATCTATGCACTTTTCTGCTTGTGGAGTATGTGTAGCTTGT
TGTAATTTGTATACCAAGGAATGGGAAGCAACTGAATAAGATTCCTGGATTTTGTGGAAGT
AGAAAGGTTGTTCCTTTGTAACTATTTGGTTGCGTATATAAGCTGTATATCGTTTGTGCTTT
GGTTTGGGTATGTTCTATCTTCTTCTCTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
TCTTAGAGCTCGAGTGCACAAATGGAATTTGGTTTCTTTAAATTTGCTGCGCAACTGTCAATTA
TTATTGGGGCACTTTCTTCACTCCAGAAAGCAATTTTACAACGTGTGTGTTTTATGTAGGCAT
CGAGGTGGCTTTTGGTTTCATCTCATACAACCTAGTCTTACTTATTTGTGATTTTGCACATCAT
GAATGAATCTGTGGGTTGAAAAAATGGAAAGGAAGCACTGCAGATGTGGTATCGACCGCTTGT
TATCAGCTTACAGCTGTGAATATCTGCTGTCTTTAGTTGCTATCGTCTGCTTCTTGTCTTCA
TACACTCATCCAGCCAGTTGTTTCAGAAAAACAGCGGCTTCTCAGTGTCAACATGCTCTCTGT
CGCTTGGTGCTTCTGTAATGCTTACTACTGCCAAAAATCAAGAATCAACAACCAAGATCTGGT
TGTTCACAGTTCTCAGTAAATTAACAGTCTACAACAATGATTATTCAGATGTGTCAGCTATGACCAAT
GAAGCAAGAACCAATTTGCAACCAAGTCTACTAAGCAATATTTGGCTACAATAACAACAGCAC
TGTCCTCAAGGAAGGAGCGGACGTAGTCCAGTGGTGCGATGCTCAAGGAATATTAGAGCAATTC
TCTTTTTTGTGTGTATTTTATCCAGACTCGTATCTTCAAAACAATGACAGGTTAATAA
CTGACTCTTAACAGTGAATGATCTAATTAAGAGAGTGTGGAGCTAGAAGTGAATGATGATC
ACTGGAGGATGGGACGATGTTTCCAGCAGCTGTAGATAAATGAAGAGGATGGTGTCACTTACA
GTTATCTCTTCTTCTTCACTTCATGCTTTTCTGGCTCACTTTATATCATGATGACCTTACC
AATCTGTCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA
AATCTCTTCCCACTTGGATTTGGCATCGTGTGTATGTTTGGACAACCTGGGACCACTTGTCT
TTACAAATCGTGATTTTGCATGAGAGCTCTAGCATAGAGTCCCACTTTGTAATATGTC
TTATTTGAAACAGATATCCCAACTTTTGAAGATTTGTGATGTTTTGTTATCTTCCCATGTAA
TCTCCAGTGTTCGCGATGAATTAGATTTTACTGCTGTGCTATTTGTTATTTCTTACCA
GTGCATGTGATATGTGAAGTAGAATGAATTCGACAGGAGAAAGTTTATGAATATGGTGTAGT
TAGTAAAGGTGGCCATTATTTGGGCTTATTTCTCTGCTCTATAGTTGTGAAGTGAAGAGTAAA
ACAAATTTGTTTGTGACTATTTTAAATATATATAGACCTTAAAGCTGTTTATGACAGCATAAA
GCAAAATGTATGGCTGCCTTTGGAAATATTTGATGTGTGCTGGCAGGAGATGCGAGAGTAA
ATGTTTTATTTTAAATTTTATAAACCAAGTCACTTAATTGGCCAGTGTGTCGAAATCTTATA
AGGTTTATTCCTGTTAGCAGGAATTTTATGAAATGAGGAGTGTGTCGAAATCTTATA
TATGAGTGGAGGTGTGCGTTATGTAATGAAATGACAGTCACTTACCAATAGTGTAGG
TGGCGTTTGTGAAGTGAAGTAAATTTTGGTCTTTTAAACTCATGAAGTATGGGTCAGT
GGAATGTTTGAAGTCACTTGAAGTTAGTTTGGGCGCAGCAGGTAGTCCACCTT
AGGAATGCTTGAAGTCACTTGAAGTTAGTTTGGGCGCAGCAGGTAGTCCACCTT
GCTTCCAGCAGCTTTGGGAGTTTAAAGTGGATATTCTGAGCCAGGAATTCAGACA
GCTTGGCAGATGTTGAACCTGTTCTATAAAAAATATCTGGCTTGGACATATGCTGTGCTC
CAGCATGAGAGCTAGTGAAGATGCTGAGCCACAGCCAAAGGTTGCAGTGAAGCAATCA
CGTCACTGCACTTACGTGGCAGAGTGAAGCCAAAAAAATATATATATTAATGAATCAAGG
AGGCAAAATTTTGAAGGAGGAAGTAGTCTGCAAAACCACTAGGTTTAGTAGGTACTTAT
ATAAATCTAGTCCAGTTCTCTCATTTAAAAAAATGAGACACTGAAATACAGACTTAAATA
GTCAGATAGCTTAATTAGGAATTTCAAGTTGGCCAATATAGCATTTCTCTGACATTTAA
AAATATTTCTTATCAAAATACATGATATGTAATTAACCTCATCTGTATATTAATGTT
GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAGATGATGGAATGTTT
AGAATAAATCTCTGCTTATATGATATACACAGTCAAAAGATGTTTAAATGCTTTTGTAT
TTACTGCCATGTAATGAAATATATAGATATTGTAACCTTTCAACCTGAAATCAAGCAGT
ATGAGAGTTTAGTTATTGTTATGTGTCAGTATGTCTAATGAAGCTTTTAAATCTACAATT
TCTTCTTTAAAAATATTTAATGATGTAATGGAATTAACAATTCAGTTAATTCGCCAACCT
TTATTCGTGTGTAGACATGTATTTCCACAAATTTGAATGGCTGTGTTTACCTCTAAATTA
ATGAATTCAGAGAAAAAATAAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
 EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
 FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
 EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
 LPKIQESQPRSGLLQSSVITVYTMYLTSWAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
 QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
 RAVDNERNRGVTYSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSWIGI
 VLYVWTLVAPLVLNDRFD

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FIGURE 42

GCGAGAAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATAACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAACAACCTCCACTGTAAGTATGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGCCAGGATTGGANGAACAACTGAATA
AGATTCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTGGTATGCAGCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTGAATG

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQORDRRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFNAFVTTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPIEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDL DLYKS
LQAWKDHKLHI DHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDKVWLLREQRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCACTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGGCCAGCCTTGGCCCTTCCGGCGGGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCACCAGCCACCATCCCCGCCA
CGCTCGCTGAAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTT
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRRAQPWFPR
RRHGLGIFHHHRHPGHVSHV PNVGLHHHHHPRHTPHHLHHHHHPHRRHHPRHAR

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FIGURE 50

GCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCTACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTTGAGAAGGGCAAGGAGTAACCC
 ATGGCCTGCACCCCTCTGCAGTGCAAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCTCTCTCTCTGGGGGAGGAGGGTTCTTGAGGGACCTGACTTCCCTGC
 TCCAGGCCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCRAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
 GCCCCGCGCCCAGT**CATG**ACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
 GGAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCTACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAACAAGAGCAAAAAGAA**ATA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

CCCGGGAACGTGTTCTGGCTGCCGACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTTGC GCCCTCACTCTCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGAAC
CTCCAAGTGGAGACCTTGGTGAGGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGAGA
CACGCTTACATACACTACAGGGGAAGCTTGGTAGATGGACGATTATTGACACCTCCCTGA
CCAGAGACCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCACATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAAC TACTGGCTAAAGCTGGTGAAGGGCATTTTGCCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCTGGGCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGCAAGCTCAAGGAAGAGAAACGAAACAGAGCAAAAAGAAATAATA
AATAATAAATTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAAGTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

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FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTGTGTTTCTTGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGTTTTTAAAGTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTTAAACAACAACCAAAAATCTATTGTGGTATGCATTGATTAACCTT
 ATAAATGTTAGAGGAACTTTACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAATAAATAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATCAAATGTGGT
 CTCTTCTGTGCAAAATGTTAAATGAAATATAAACATTTTTTACTTTTTTAAATATTCGGTGG
 TCAAAATTCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGCACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCCCAATACTATTGCTTCCATTGCTGCTGGTGAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCACCACCTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTG
CTCGCATTTTGGCTTTTCGTTGGTTTACAGTTGGCCCTTTGGATCTCTGATTGCATCTATGTGG
ATTTCTTTTTGGAGGTTATGTGTCTAAGAAAAGACATAGTATACCTGGAATTGCTGTATT
TTTCCAGAAATGCCTTATCTTTTTTGGAGGGCTGGTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCCTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTAATAATTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

G G G A G G C T G T G N C C G T T T T G T T T T N T T G G C T A A A T C G G G G A G T G A G C G G C C C G C G C G
C G N G A C A C C G G T T C C G G G A A C C A T T G C A C G A C G G G G T G G A C T G A C C T G A A A A A A T G T T T G
G A T T T N T A G A G G G C T T G A G A T G C T A G A A T G C A T T G A C T G G G G G A A A A G C G C A T A C T A T T
G C T T C C A T T G C T G C T G G T G T A C T A T T T T T T A C A G G C T G G T G G A T T A T C A T A G A T G C A G C T G T
T A T T T A T C C C A C C A T G A A A G A T T T C A A C C A C T C A T A C C A T G C C T G T G G T G T T A T A G C A A C C A
T A G C C T T C C T A A T G A T T A A T G C A G T A T C G A A T G G A C A A G T C C G A G G T G A T A G T T A C A G T G A A
G G T T C T G T G G G T C A A A C A G G T G C T C G C A T T T G C C T T T C G T T G G T T T C A T G T T G C C C T T T G
A T N T C T G A T T G C A T C T A T G T G A A T C T T T T G A G G A T T A T G T T G C T A A A G A A A A A G A C A T A G
T A T A C C T G G A A T T G C T G A T T T T T C A G A A T G C C T T C A T N T T T T T T G G A G G G C T G

TACGCGCCGGCGT**GAT**TTCGGCTTCGGCTGGTGTGCTCTGGCTGTGCTGCTGCTGCGCGCTC
TCTCCAGAGTTTATTTGGGACTTCTTCGGCAGCTCCCGAATCTTCTTCCGAAGATGT
AAACGCGCTACGCGCGCTGTGTAATCGACAAGGCGCAGGAAGAAGTTCTCAAAACAGC
TTTTTTCAGCAACCAAGTTCGCCGGAAGCTGGATGTGTTGGTAAATGGCAGTGGCTTTGGGG
CGCTTGGCTCGAGCTGCAATTTAGCTTAAAGCTGCAACGCGATCTCTGGTGTCTGGAACAACAT
ACCAAGGCAAGGGGGCTGCTGTACTACTTTGGAAGAAATGGCTGTAAATTTGACACAGGAAT
CCAAATACATTTGGCGGTATGGAAGAGGCGACATGGCCGCTTTATCTTTGAGGACAGTCACTG
AAGGCGACTGGACTGGGCTGGCTCCCTGTCTCTCTTTGACATCATGGTATCGAAAGGGCCC
AATGGCCGAAGAAGGATACCCCATGTACAGTGGAGAGAAGGCTACATTTGAGGGCCCTCAAGGG
CAAGTTTCCACAGGAGGAAGTATCATTTGACAATTTATAAAGCTGGTTAAGGTGGTATCCGA
GTGGAAGCGGTATCGCATCTCTGTGAAATTTCTCCCATTTGCCCTGGGTTCAAGCTCTCGAC
AGGTTGGGCTGTGTACTGTTTCTCTCATTTCTTCAAGCATCCACCAGAGCCTGGGTGTA
GGTCTCGACAGCTGCGGGGCTCTCTCTGAGCTCAGGCGAGTACTGACATGCACTTTCCCCA
CTTACGGTGTACCCCAACACAGTGGCTTTTCCATGACGCGCCTGTGTGTCAACCATAC
ATGAAAGAGAGGCTTTTATCCCCGAGGGGTTCCAGTGAATTTGCCCTTCCACACCATCTCCCT
GATTACGGGGCTGGGGGGCTGTCTCCAAAGGCCACTGTGCAGAGTGTGTGTCTGGACT
CAGCTGGGAAGAAGCTGTGGTGTTCAGTTGAAACAGGGGACATGAGCTGGTGAACATCTATTGG
CCCATCTGGTCTTCCAAGCAGGACTGTTTCAACACCTTGAACACCTTACTGCCGGGGAAGCGC
CCGCTGCCCTGCCAGGTGTGAAGCAGCAACTGGGGACGCTGGCGCCCGGGCTTAGGCATGACCT
TGTTTTTATCTCTCGCTCGGAGGACCAAGGAAGACCTGCATCTTGGCTTCCACCAACTACTAT
TGTTTACTATGACAGGCAATGACAGGCGAGTGAAGCGCTACGTCTCCATGCGCCAGGGAAGA
GGCTTCGGGAACACATCCCTCTTCTCTTCTTTCGTTTCCCATAGCCAAAGATCCGACCTGGG
AGGACCGATTCCGAGCGCGGTCCACCATGATCATGTGATACATCCCATGCCCTACGAGTGGTTT
GAGGAGGTGGCAGGCGGAGCTGAAGGGAAGCGGGGACGTGACTATGAGACTCTCAAACAT
TTTTTGTGGAAGCTCTATGTTCAGTGTCTTGAACATGTTTCCACAGCTGGAGGGGAAGTTGG
AGAGTGTGATCTCAGGATCCCCACTCAACCAAGTTTCTGATCTGGCTGTCTCCCGAGGTCGC
TGCTACGGGGCTGACCATGACCTGGCCGCGCTGACCCCTTGTTGTGGGCTCTTGGAGGCG
CCAGAGCCCCATCCCCAACTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGTCTG
GGGCGCTCGAAGTGGCTCTGTGTCGAGCAGCGGCATCTGAAGCGGAATCTGTACTCGGAG
CTTAAGAATTTTGATTTAGGATTCGGGCGCAGAGAAGAAAAGAT**TAGT**TTCCATCAGGAGG
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTTCTTCTGT
CATTAGTTCTCTGACAGTTATAAAGCACTCTAATTTGGTTGTATGCTTGAAGAGAGGCTCTAG
TTTTAAATCACAATTTCCGAATCTGGGGCAATGGAATACATGCTCTCCAGCTGGGGCAGGTGAGA
TCTTTACGGCTTTTATAACAATGCCATCCCTCATTAATAGGATATTGATCTGAGTGTGATG
ATCATGACGAGCGCGCGCTCTGCATCCCTCAACCATGCCTCTCAACTCAGTATCAAGGACG
TCTATTCATCTGTGGATAGAACCCTGGCAGTGTGTGAGCTCAACCTGTGGGTTCAGTCT
TGTCTGTGAGGCTTCTGCTCTCATTTATGTAGTGTACGCTGACGTTCTATCATCTTCCAG
GAAGAAGGAGACTTAATGAGGCTTTCTTCAAACACTGGGGGTGGTGTGCTGCTGCTCATTC
GGTTTGGGAGAGCTCATGATCTCTTTTGTGCTGTTTGAAGAGCTCAGGAGTCCATCAGTTATGA
CGGTCGATCTCTGAGGCTTATCAATCAATTTATGGAAGTCCCGGCTGTCTCTCTTATCA
CTTATCGCAAGTGGTCTCAATGTGCCACAGGGAATCAGTACTCTGAGCTCAATCAAGC
CTTATCGCAAAATCAACAGGGAAGGTGATGCAAGGGAAGGTTGACATCAGGAGTCAGGCA
TGGACTGGTAAAGATCAATACTTTCGTGGGCTGAAGCAGGCTCAGGGGCACTCCAGCGCAAGG
CACAGCAGGGACACTCAGGGAAGTGTGGGTAAGGGAAGGAACTCACATCAAGAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCAATTTGCAAGTTAATTAACGACATGTAGGG
TTAGACGTGTAGTGAATGCAAGCTCAAGTTTGGAAAAATGACTTTTCAGTTATGTCTGTTG
GTATCAGACATCAAGAAAGGCTCTTTGTAGTTTCGTGTTAATGTAACATTAATAAATTTATGT
ATTCCATTGCTTTTAAAAAAGAAAAA

FIGURE 64

MWLPLVLLLA VLLLA VLCKVYLGLFSGSSPNPFSE DVKRPPAPLVT DKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIDKYIKLVKVVS GAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHEL VNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYYVYYDTDMDQAMERYVSMPREEEAAEH
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEEWQ AELKGKRGSDYETFKNSFVEA
SMSVVLKLPQLE GKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

[illegible]

MRVRIGLTLLLCVALLSLASASSDEEGSQDESLSKTTLTSDSESVKDHTTAGRVVAGQIFLD
SEESLESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKVKRKALTAIEGTAHG
EPCHFFFLFLDKYEDECTSDGREDGRLWCATTYDYKADEKWKGFCTEEEAARRQMQEAM
YQTGMKILINGSNKKSKREARYRLQKASMNHTKALERSYALLFGDYLQNIQAAREMEFK
LTEEGSPKGQATLGLFYASGLGVNSSQAKALVYTTFGALGGNLIAHMLVLSRL

CTTCCACAGCCCTGTGCCCAAGACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGACCTTCC
GTCAGTTTCCCAGACAGTCTTGCCCAAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCTTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCTGTGTGACATCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCTCCCCCTCTGCCTCCCATTTCT
GCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 69

GCGGCCCGCCCGAGACCGGGCCCGGGGCGCGGGGCGCGGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGCAGCGCGCGGGCCCGGCCCTGACCCCGCGCGCGCGCGCGTGAAGCCC
 CCGCCGAGGATCCCGACAGGCCGAGATGACGCCGAGCCCGCTTGTGCTGCTCCTGCTGCCCG
 CGCTGCTGCTGGGGGCTTCCACCGCGCGCGCGCGCGCGGAGGCGCCCAAGATGGCGGAC
 AAGGTGGTCCACAGCGAGGTGGCCCGGCTGGGCCGCACTGTGCGGCTGCACTGCCAGTGGGA
 GGGGACCGCGCGCGCTGACCATGTGGACCAAGGATGGCGCGACCATCCACAGCGCGCTGGA
 CCGCTCTCCGCTGCTGCCGACGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGCG
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCGCTGAGCGTCAACTACACCTCGTCTGT
 CCTGGATGACATTAGCCAGGGAAGGAGAGCTGGGGCCCGACAGCTCCTCTGGGGGTCAAG
 AGGACCCCGCGAGCGAGTGGGACGACCGCGCTTACACAGCGCTCCAGATGAGGCGCG
 CGGGTGATCGCACGGCCGTGGGTAGCTCGGTGCGGCTCAAGTGGCGGACGCGGGCACCC
 TCGGCCGACATCACGTGGATGAAGGACGACCGGCTTGAACGCGCCAGAGGCGCGTGAAG
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCGCGGAGGACAGCGGCAAAATAC
 ACCTGCCCGGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA
 GCGGACCCGTTCCAAGCCGTGCTCACAGGACGACACCCGTGAACACGACGGTGGACTTCG
 GGGGACCGACCTCCTTCCAGTGCAAGGTGCGCAGCGACGTGAAGCCGGTGATCCAGTGGCTG
 AAGCGCGTGGATACGGCGCGCGAGGGCGCGCAACAACCTCCACATCGATGTGGGCGCGCAGAA
 GTTTGTGGTGGTCCCGACGGGTGACGTGTGGTTCGCGGCGCGGACGGCTCCTACCTCAATAAGC
 TGCTCATACCGGTGCGCGCGAGGACGATGCGGGATGTACATCTGCTTGGCGCAACACC
 ATGGGTGACAGTGTCCGACGCGCTTCTTACCGGTGCTGCCACGACCAAAACCGCGGCGCC
 ACCTGTGACGCTCCTGCTCCTCGGCACACTAGCTGCGGTGCGCGTGGTCACTCGGATCCAG
 CCGCGCTGTCTTATCTGCGGACCCCTGCTCCTGTGGCTTTGCGAGGCCAGAGAAGACCGG
 TGCACCCGCGCGCTGCCCTCCTCCTGCGCCACCGCGCGCGGAGCGCGCGCGCGCGCGG
 CAGCGGAGACAAGGACCTTCCCTCGTTGGCGCGCTTACGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGAGATGGGTCTCGGCGAGCCCCAGCAGCTTACTGGGCGCGGCGCGGAGTGTGGTGG
 CCTAAGTTGATCCCCAACTCTACACAGACATCCACACACACACACACACACTCTCACAC
 ACACCTCACAGTGGAGGGCAAGGTCCACAGCACATCCACTATCAGTGTGAGACGCGACCGT
 ATCTGACGTGGGCGCGGGGGGGCGGCCAGACAGCGAGCTGGGAGGATGGAGGACGAGCTG
 GCAGCAAGAGCGAGGGGACCATGGCGAGGAGGAATGGCCAGCACCCGAGGAGTCTGTGTG
 TGAGGCTATAGCCCTGGACACACACACAGACACACACTACCTGGATGCATGTATGCAC
 ACACATGCGCGCACAGTGTCTCCTGAAGGCACAGTACGCACACGCAATGCACAGATATG
 CCGCTGGGCGACACAGATAGCTGCCAAATGCACGCAACGCGACAGACATGCCAGAAC
 TACAAGGACATGCTGCTGAACATACACACGCAACCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACACGATATGCTGTCTGGACGACACACGTCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATATGCTGCTGACACACATGCACG
 ATATGCTGGACACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGACAC
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACAGTGCACAGGCGAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTCACACACACACGCGAGCATGCTGTCCGACAC
 ACACAGCATGCACAGATATGCTGTCCGACACACACACGCGACAGATATGCTGCTGGAC
 ACACACACAGATATGCTGCTCAACACTCACACAGTGCAGATATGCTGCTGGACACACACA
 TGTGCACAGATATGCTGTCTGGACATGCACACGTCAGATATGCTGCTCCGGATACACAG
 CACGACACATGCAGATATGCTGCTGGGACACACTTCCGACACACATGCACACACAGGAT
 GCAGATATGCTGCTGGACACACACACAGATATGCTGCTCAACACTCACACAGTGCAGT
 TATTGCTGGACACACATGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATA
 TGCTGTCCGGACACACAGCAGCAGACATGCAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGCACACAGGTGCAGATATGCTGCTGGACACAGCAGCTGAGTGTCTTTGG
 GAGGTGTGCGGTGAAGCTGCAGTACGTGTGCGGTGAGGCTATAGTTGATGAGGACTTT
 CCGCTGCGCCGCTCACTCCCCAACTCTGCGCGCTCTGTCCCGCTCAGTCCCGCGCTC
 CATCCCGGCTCTGTCCCTGGCTTGGCGGCTATTTTGGCCACTGCTTGGTGGCGCAGG
 AGTCCCGCTACTGCTGGGGTGGGGTGGGGGACAGGACCCCAAGCGTGAGAGGCTGGAG
 CCGATGGCTATGGCTCATCCCCAGTGCATTCTCCCGTGACACAGAGAAGGGGCTTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATATGATGGAAGAGAGCTGGGTTCGAGGAC
 TGTGGTCTTCTCTGGGCGCGGACCGCGCTTCTTACGCACTGCTGATGACACACCCCG
 GTCCAGGCGACACACACCCCGCCCACTGTCTGTTGGGCGGACGATCTGTGATATTTA
 TGTAGAGTTTGAAGTGAAGCCCGTATATTTAATTTATTTTGAACACCTTA

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FIGURE 70

MTPSPLLLLLLPLLLLGAFFPAAAAARGPPKMADKVVRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLLDDISFGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARFVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKFVL
TGTHPVNTTVDFGGTTSFQCKVRS DVKPV IQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTHSHTSHSHEGKV
HQHIHYQC

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ACGACTGAGGAGCCCTGGAAAGACACGGTCACTGGGATCTGAGAAACTCCAGGGGACGACATTCCAGAGTC
AGTACCTGTCTGAAGACCCACATCTACCTTTCGATTTTCCACGGGCTGGGGGAAAGATGCTGGGGACGA
AGGCTCGGGTGTCTTCTCTTCGGTCTGGAAGTCAATCTGTGTGGGGAGACAGCATGTGTCACCCAGTCA
TGAAAGAAAGTTCAGGCTGGGAGGAAGAACCCAGCATCTTTGCCAAGCTCGCGACACCOGTGACCGGCTGG
TGAGTGGACAACTGTGTCAAACTCGCATACCCAGCGGGGAAGGGCAGTATGAGCGGCTGAGGCGCACTTCGCT
TCTACTATGGGGACCTGTATGTGGCGGCTCGGCTGGGTAGAGGTCTGACGCCATGACATGGACACCTGGGCG
GAGGAGTGGGAGG
GAGTCTGCTCTTAATTAACCTGACCTGAGTCTCTCTGCCACAGGATCGCTCGGCGGACAGACAGGAGCATCTGA
GCCCATGTGCTCTCCCTGGAGCAAGTGCTCAGTGCCTGTGGTGCAGTGGGGTCCAGACTCGCACAGCAATTTGC
TTGGGACAGAGTGGTGTCCGCTGTGCAGTGAAGGCGAGGAGAGGCTCAGCATGCTATGGGCGAGGACTGTACAG
CTGTGACCTGACCTGCCAAATGGGCGGCTGAATCTGTACTGTGTATGCTGCTGATCGCAGGACTTCATGCTTT
ATGGGCTGCTCTCCCTCGGAGGTCTCCAGGCTCTCAGGCTGAGTGTACTATCTCCCTGACACAGACAGCTGG
GAG
GATGCAAAAGGTCAAGTTTGGCCCATTTGTAATCTACAATGCCAAGCTCGTGAAGGACGACCAATCAAGG
CAGAGTTTGTGGAGGACAGACTTCATACATGTGTGATGACCTGAGACAAAGCCAGGAGAGCTGGGCGAGCG
TGCTCTCTGTGCTGTGAAGGCGACAGGGAAGCCGAGCAGACAAGTAATTTTGGTATCTAATATGACAAATTTGCT
GGATCTCTCCCTCTAGCAAGCATGAGAGCAAGCTGGTCTGGTGTGAGGAACTCGACGAGCCAGCGCTGGGGAGTACT
TTTGGAGCGCCGAGTGTGATGCTGGGGTGTGAAGTGTGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCT
TTTGGAG
TGTGGAAGAGGCCATCACTTTGAAGAGCTGGAGACAACATCATCCCCCTGGGGAGTGTGGTGTGTGAAGCC
CCATGGTGTGAAGTGGAGTTTCATCCAGGAGTTTCTACAGCCAGAATGGGGAGGCCCTACATAGGAAGAAGTGAAG
CGCGTGTGACCTCTCTGATGCCGCGGATTTTCCACAGCCACAGCTGCCAGCATGACCTGAACCTTCATCACT
TGACGAAGGAGAGCTTTCCCCCTGGGAGCTATGGCAATGTCTCTCGGACTTGAAGTAGAGTGTGTGATGAT
GGAGCAATCAAGTCAATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GGAGCAAGGAGGAGTCAATCAATACAGACAGGCGCTGGGGAGGAGGAAGTGTATTTCABATTTGAATTAAGA
GGAGGACAAAGAGAGAGACAGAACTCTCTGGTGGGCAACCTGGATGATCTGTGAGGAGAGGCTCTTTAAATCGG
ATGTTCTTGAAGAGCAGCGGCTGCTTTGTAAGTGAAGGCGTACCGAGTGAAGGTTCTGCTGTGTGAGGAG
ATCCAGGGGGTTTGTGATCTCCGTGATTAACCTGGAGCTAGAGACTGGCTTCTGTCTCCATCCAGGCTCGGG
CCGCTTGAAGTCTCATCAGAGGCCGACAGCGGGCTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GAG
CCAAATGACAGTTGGCGTCCCTCAGGCTATCTCAACAGCTCAACTACGCTCGGACGGACCATGAGATCCAG
GGTTAAAGAGCAATGTTTCAGATTAGATGGGCAAGCCAGGCGCAACTCAGCTGAGGAGAGCAATGGGCGCA
TCTATGCTTTTGAAGAACCTCGGGGATGTGAAGAGGCCAACCAGCTGCAGCGCACTTCGGTCTTCAACAGATT
GGGGGGATGATATGACTACACACAGCTGCCCTTCAAGCAAGCATCTATGAGCTGACCTGAAGATGAGGAG
GGGATGCTGGGCGGAG
GAG
AGCATCTGGGACGGGAGGACGCCAATGTCATGCTGCTGTGGGATTCAGTGGAGCTGGGATGCTCTATGA
TCAGGACAGGCTGTGAGCCGCACTTGTGAAGGATCTCCCGCAGGGCAGCTGCCGCTCAGGACAGCTGTGAAACCCA
TGCTGCATGAGTAACTGGTCAACCATTTGCCACTTGCACTGCAACAGCAAGCACAGTGTAGTACACATCTGGGCA
CCCTTGGACCCCACTGGGCAACATATGGCTCTACATCTGCAAGCAGGAGCTGCAAGGAGGAGGAGGAGGAG
GAG
TCACTTTCAACTGTGTAGAGAGGCAAGTAGGGCGCAGAGTGGCTCCAGTACTCCCAAGCTCCAGCGGCC
TCCGCTCTGCGAGGCTCTCAAGGGAAGTGTCCGCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
CAGGCTGGAGTGTGGCTCTCTGAGATTCTGAGATTGCTGCAAGCGCCCTGATCAAC**TAA**GTTTGTGTGCT
ACTTCAACCTCTCTCGGCTCTATTTCATGTGAGCAGGCTATGTGAGCATGATGCACAAATCTGTACCTGTGAT
TTAAGCATCTGTGTTTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
GGGATCTGAG
GGGCATCTGTAAATCTCGACCTTCAACTGTACTTTTAAATGCCATTAATGCAAAATATACTCTCTCTTCT
TTTCTGATGGTTTGGCCACTCTGCAATAGTGAATATCTGTATGTGATGTGAAGTCAAAATCAACCAATTAAGATAT
TTCTTGGCTTGTCTCCAGGACATAGGCAAGCTTGATCATATTTATCATCATATAAAAGTGTGTGAATTAAG
AATAATAACAATAATCTTATCTGAATGTAAATAACTATTATTCTTGTCTGTAATAATTTGAATTTGTAGCT
TGTGATGAATTTGAATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGAT
TCCTCATCTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGAT
CAGTGTAGCCAGGCGAGATGCTAATAATGATCATCTGTAATTCGAAATTC

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLES PGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGS PREGFWCLNREQ
 RPPGQNCNYSYTVRFLCPPGSLRRDTERIWSWPSPWSKCSAACGQTVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDS DGRFRI PGLCPDGKS ILKITKVKFAPIVLTMPKTS LKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCKCATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRLQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFPVPESYLIRLPHDCFQONATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSQRC TETR SI VRGRV
 SAADNGEPMRF GHVYMGNSRVSM TGYKGTFTLHV PQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPIT LEAMETNII PLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTD LNFINDEGDTFPLRTYGMFSVD FRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR
 VKKTAFIQISMAKPRPNSAESNGPIYAFENLRACEEAPP SAAHFRFYQIEGDRYDYNTVPFN
 EDDPMSWTE DYLA WPKPMEFRACYIKVKI VGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVI PQGSCRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVNGVALT
 FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

ATCGAAGTTTGTTAAACGCTACACACAAGTATGTTGGGCTTCACCAAGAGTCCTCAATATAGTGTAATACGACCA
AATATCTTCAACTCTTCATATTGGTTTGGGATCTGCTTGAAGCCCATCTTCATTAAAAAAAATACAGAG
ACCTACCTACCCCTAGCCATACATACATATGTGATATATGTAACATAGACAAGATCCGCAGATACATAAGCG
AAGCTTCGCTTTAGTTTCCAAGAAATATACAAGAAATTAGACATGTAATTTGCAAGTCCCTGTCGATTCTG
CCCTTTGGGTTACGGTGTCTCAGTGATGTCAGGCCATACCTTTGGTTGGGGACATTTGATTTGTGTAAGACT
CAGATTATTACCGGAAGAGGGAAGTTGGGGATTACATGGCTCGACGCGGAATTCCACGCAATGACAAAAATA
TCTGAAAGTGAACCTCGATCTCCCGGATATACCTGTGAGACCCCTCTGAGACGTTCTGTGCAATGGGCATCT
CTCATGTTGCAAAATAGATGTGATGTCGGAGTACCCCTGAGCTGGCAGCCGCCCTGAGCTGATGTTGATTT
GAGGAAGACATCTCCCTCCACATTTTGGGACGTGTCGCATTGTGAAGAGGATATCCCAAGCCTCTCCAGTTAAAT
CACTCTGTCTTGGAGCAAAACATTTGAGTATACAAGACACATAGTTATTACCTTTGAATCTGGGGCGTCACAGC
AAATGATCTCTGGAGAGGCTCTCGATTATGGACGAACATGGCAGCATTACGATTATATGCCACAGACTGCTTA
GTAGCTTTTTCACATGGTATCTAAATTCGTGAAGGATTTATACAGCATACGGTCTTGAAGATCTTTGACAGCA
AGAGTACTACACAGGGTATACAAACAATAGCAAAATATCACTTTGAAATCAAAAGCAGGTTTCGGCGTTTGTG
CTGGACCTTCGCTACGCAATATGGCTCTCCCTCTACGCGACAGCTGGATACCAACCAAGAAAGTACAGAGATTCTTT
ACAGTCACAGACCTGAGATAGGCTGTGTAAGCACGCGTTGGGGAAATTTGTTAGATAGAGCTACACTTGGC
ACGCTACTTTTACCGGATCTCAGACATCAAAAGGTGCGAGACAGCTGCAAGTGTAACTCCATCGCACTGTAGATG
TGTATGACAAACGAATTCAGATCGCAATGTGACAGCAAGCTTACAGGTCCAGACTGTGGGAATCGCAAGAG
AATTTATCAGGCGCAACCTTGGAGTCAGGCTCTTATCTCCCCATCCCCAAGGCACTGCAAAATCTGTATCCC
CAGTATTTTCAGTATTTGGTACGAATTTCTCGACAAACAGCTCTCTGACGTCGCAAGCGAGGAGGACGTGCCA
CAACGTCGCTGCTGCTGTCGCGCGCCGCTACACCGGCACTCTCTGCGAGAAGCTCGGCTGCGAGGAGCTGCT
AGCTCGCGCTGCTGCTGCGACGGCGCGCCGCCACGCGACGCCATCCGAGCTGTGCTGCTGACACGCTGCTG
GGAAACCCGCGACCCCTGCTGTTTCTAGTGTCACTCTCAGGCCACCCGACGCGGCTGTGCTGCTGGGGAACCA
GACAAACCCCAACATTTGTCTATAGTATAGGAACACACATACAGCAACCCCACTCAGCAGATGACAAAA
CTAAGAAAGGCTAACTGACTTAAGCATATTTATTCACCTGGGACAGCATACCCGAGTCAAGACTGTTAATTT
TGACTTCAGAGGATGGGCACTTGTATATTACTGCAAAATCACAATTCGACGTCAGAGCATATTTGTGGA
TTGGAAGAGCTGCGACAGCCCCCAACAGCAGAAAGCAAAAAACAACAAATCAACCGCACTAAAAACATTTGGC
TACTCTAGCTGTGTGGCCCTAGTAGCAGCTCCGCGCAATGTGTGGACCAACAAATAGCATTTTGGCTGTCAG
GTGCTATTGTGGGATAAGGAAATCTGTGTTACAGCTGCCATATTGGCCTGCTCCGCTCCGCTGATCCCTGCAAC
TGTGCTTTTGTAGAGCTGTGCTCTGTAACTCTGTTGGTTGAAAGATTTCTTGTCGTATGTGTAGTAGTCCAA
TGTTGTAAACAGCCOCTCTAAAGAGCGAAGCCATACCTCCCTGTATCTTAGCAGCACTGAGTCGAGTCGGA
GCACACCCCACTATACAGAGTGCGCTATAGGAAAAAAGAAAGTGATCTATCTCTTTGTTATCAATAGAGTT
ATTTTCTTTGAACTATGATATATGATATTTTGTATATTGCAAAATTTGTTGTACCAACAACTCTGTAAT
GTATCTAAATCGAATACGAAAGACTGACATTTATTTGTCTCTTCTGCTTTTGTGTTTGTGTCAGTCGAGA
GATTTCTTTGATAGGCGACAGAGCTGCTGGCATTAAGCAATACAGTTTACATATATACAAAGTGTAAATGA
TTCACCAAGGACATCTTAATATTTGCTTTGTGCTTTAAGATCGGAAGATTAAAGAAATAAAACCTCTGCA
TAAACGATTTTCAGAAATTTGATATGCAATTTCTTAAGATGAAGGACAGCCACAGCAAGCTTTTCACACTCT
TTACTGATTTCTGCTGGACTGAGTACATTCAGCTACGAATTTAGTTTCCGAGGAAGTGGATTTGATCTTCA
AGCTTGCGCAACTCTTGCAAAATATGAGACTATTTCCACTTGGGAAAAATACACAGCAAAAAAATAAAAAA
AATATAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGCKKNYQGRPWSFGSYLPPIPKGTANTCIPSISISIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTLLGTAS
PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTT
 CTCTTGTTGGACCATGTCCGTGATCTTTTTTGCTGCGTGGTACGGGTAAAGGATGGAGTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGGCAGCTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTTCTTTGCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCTGTGGTGGGAATTCACAGCTTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACCTTGAGGCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTGAGGAGTTACCTTTGCAGAACATTCTTTACAGGATCCAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGCATGTCAGTGAAATCTGGGAATGGCTGGATTGCGAAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTACATTTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTATTTCATGAATCATTCATATGATTTGATCCCCAGGATTCTATTTGT
 TTAATGGGCTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTACATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC
 TAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTAAAAAATAAAAAAAAAAAAAA
 AAAAG

MSVIFFAFCVVRVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVVK
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

[illegible][illegible]

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTGTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACAGAGGCGGGTGGT
 CCTGCCCTTTAAGGGCGGGCGCTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTCCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGGCGGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGT**A**
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGAC
CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATGGCCTGGGTGCTGTCTCTGCTCCTGCC
TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACACTACTACATCCAGTGGCT
CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
TCCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTGTCTGGCTCCAGAAAG
GGTGCTCTGGCCGGGTCTATGAGACAGTGGTGATGTTGATGCTCTCTCACTCTGCTGGTGCT
AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTCTTGGGGTCTG
CTGCTCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGGTCTGACGG
 GCCTGTCTGTGCTCAATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCAATCAGGTTGTACTCATCTTTACCTAATGGTGTCTCAGTTGTGGGCTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGCAGACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGCAATTTCTACA
 TTGTGTTCTCTACACGCAGCCTTTGCAGGCCCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTGGGCTGGACAGACTGCCGCTGCCGT
 CTCGGTTCCTCCCCAGGCATCTAGGAAGACCCAGCACCAG**TGA**CTCCAGCTGGGGTGGGA
 AGGAAAAAACTGGACACTGCCATCTGCTGCTTAGCCTGGAGGGAAGCCCAAGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGAGCAGAGCCATCTGCATATT
 GCATAATCTGAGCCAGAGTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACTGTGGCCT
 CAGCATGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGCCATCCCATAGCCATGTTTACATGATTGATGTGCAAT
 AGGGTGGGGTAGGGGCAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 TTTGCCTCTGGCCACGACAGGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG
 AAAGACCAAGGGGATAGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA
 AAAAA

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHI FLTRFKKPAEFTTVDDDEATVVK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYI QWLNGSLIHGLWNLVFLFPNLSL
IFLMFPAYFTTESGFGAGSRKGV LGRVYETVVMMLMLTLLVLVGMVWVASAIVDKNKANRESL
YDFWEYYPYLYSCISIFLGVLLLLVCTPLGLARMSVVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPDLMELLHRQVLALQTQRVLEKKRRKASAWQRNLGYPLAMLCCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMGQTSLGQVSFSKLGSGFAGIVQVVLIFYLVMSSVGVGY
SSPLFRSLRPRWHD TAMTQI GNCVCLLVLLSALPVFSRTGLTRFDLLGLDFGRFNWNLGNFY
IVFLYNAAFAGLTTLCLVKVTTAAVRAELIRAFGLDRPLPLPSVGFPQASRKTQHQ

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTG
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTT
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGCTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

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FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCAATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTTCAAGATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACCTCTGGGCTCAAGTGATCTGCTCACCTTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCCGACCAGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAGGACCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAC TAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCGGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACGAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAAGTTTGACAAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAAGAGAGGAAGCGAGAGAAGGTATCAAA
 CAGTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCGGCCCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATCAAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTAA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKALQLHPDRNPDDPQ
 AQEKFDLGAAYEVLSDSEKRRKYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTTPRQQ
 DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
 MTQEVVCDCECPNVKLVNEERTLEVEIEPGVRDGM EYFFIGEGEPHVDGEPGDLRFRIKVVKH
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAACCCGGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGNGTGCACCGAA
GCGCGGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCTNGAAGTGCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCTGATGATCCACAAGCCCG
GAGAAATTCCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACGCC
 TTGGTGCTGGTTTGACGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGCCAAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCAG
 TCACCTGGTGCTGGTGACAAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCCAGGCCCTGAAGGCTTCTGTCAGGAGCAGTCTGCAATTT**TAG**TGCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCGGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCCTCTTTTGCAAGTTCGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAATAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAAATG
 TGTGGCAATTTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTGTACTCTCTCACCTGGCCTGTTTCATTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTGCAAGTTTGGGTTTGAAGCTGAGGAAT
 ACAAGTTGATGATTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCTGGGCTTCCGAGGTGCTTTCGCCGCTGTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTTCTGTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATTGGTTTAGAAAGAACATTAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
GGGCTTCTTCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
AGTGAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAATTTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAAACGTATAG
CCTACAAAGTACCAGCAGCAAAATAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTGTAGAAGTGCCACTGCAATGGCAAAAATATTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTAAAGTATTAAAACCAAGGAAACCCAATTTTG
ATGTATGGATTACTTTTTTTTNGCNCAGGGCC

FIGURE 90

MISLTDTKKIGMGLTGFGVFLLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSEVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59



FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTGAGATCTTCTTCCAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGC TGCCAGGAAGGAGACGCCTTCTGAGTCTGGATCTTTCTTCTCTGGAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGACCTCGCGGGACTGC
 TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
 ATCAACACCATTAGCTCTTCACTCTCTCTCTGGCCCATTAACAAGCAGCTCTTCCGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTTCACGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCAA
 TTATCGGCTGGATGTGGTACTTCAACGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGACGACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT
 GATTCACTGTGAGGGCACACGGTTACGGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCACTGTATATGACTGTACACTCAATTTAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTGTATG
 TTAGGAGGATCCCATGGAAGACATCCCTGAAGACGATGACGAGTGTCTGGCCTGGCTGCAC
 AAGCTCTACGAGGAGAAGGATGCCTTTTCAAGGAGGAGTACTACAGGACGGGCACCTTCCAGA
 GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAACTGGCTGTTTTGGGCCTCGC
 TGGTGCTCTACCTTTCTTCCAGTTCTTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATTCCGAAGGGAACCTTGGGGAACCTGGTGGCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACGAAGGGGACAAGTTCCCTTTTCACTCCTTTGGTGCTGAGTTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTGAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
 CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFATVRSRLRNVS AVYDCTLNFRNNENPTLLGVNLGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRMMIGVTEIDKGSAYGNSDS
KQKLND

93/330

FIGURE 94

CTGAGGCGGCGGTAGCATGAGGAGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
 CGGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAAATCCGTCGTCATTGAGATCAGATCATGACGTTTTAGAGAGAGGCTGCTTCACAA
 AAACCTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGTTACCTTTAGTGGTTGCCAATCTGGGCATGCTCTGAACAACCTGGGTATATAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAATCCAAAAAGCCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCCAATTTCTGAATTTCTTCATTGATGTTATGCTTTAAAAATAGACA
 TGTTCCTAAAAGTAGCTGTAACCTACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCTACA
 TTTTGAATCCTTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCAATTTGTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCAAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTTCTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEVKGEAKNSITDSQMDDVEVYTIIDQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSPLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSI CKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDWRQFKRSRLDQTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

FIGURE 96

GGCACAGCCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCGCAGGGCAGC
 CCAAGCAGCGCGAGCGGAACGCCGCGCGCCACACCCCTCTGCGGTCCCGCGGCGCCTGCCACCCCTCCCT
 CCTTCCCGCGCTCCCGCCTCGCGGCGCAGTCAGCTTGC GG GTTCGCTGCCCGCGAAACCCGAGGTACACA
 GCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCCTCCAGGCCCTCCTTCTCCCTGGCCGGCGCCTGGCACCC
 GGGAGCGCTTGCCTGACGCGAGGCCAGCTCTACTTTTGC GG CGGCTCTCCTCGGCTGCTCGCCTCTTCCAC
 CAACCTCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCGAGCCCTCGGCGCGCTGCGCGTAGC
 CGCGCTTCCGCTCGGCTCCGAAAGGTGGAAACGCTCCGCCCGGCCCGCACCATTGCGCAGGTTCGCGCTGCC
 CGCGCTTCTCTGACACCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCGGAGCTCAAGTCGAAAGTGTCTCGG
 AAGTGGCAGCTCTTTACGTGCCAAGGCTTCAACAAGACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGCTCCCGAGGTTTCTACTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTCGAAAGTAAAGA
 TGATTTCAAAGTGTGGTGACGCGAACAGTGAATCATTGCAAGCTGTCTTTGCTTACGTTACAAGAGTTTG
 ATGAATTTCTCAAAGAACTACTTTGAAATCCAGAGAAATCCCTGAATGATATGTTGTGAAGACATATGGCCAT
 TTATACATGC AAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT
 CGCAAAATGAAGTCCAGGTTACTCGTGCTTTGTAGCAGCCGTACTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGCTGCTGAGCAAGTCTCGGTGGTAAACCCACAGCCAGTGATCCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGCTCGTGACTGTGAAGCCATGTTACAACCTACTGCTCAAAATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGGGCTAGA
 GGGTCTTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG
 ATAATAGTGTTCAAGTGCTCAGAAAGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAAT
 TCTCGTCCATCTCTGAAAGTGCTTCAAGTGCTGCTTCAAGCACATCAGCCCGAGGAGCGCCACACAGC
 AGCTGGCACTAGTTTGAGCCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATCTGCTGCT
 CCGTTCGAGCAACGTTTGCAACGATGAGAGGATGGCTGAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACCTGTTTCAGTGACAGGAAATGGATTAGCCAAACAGGGCAACACCCAGAGGTCCA
 GGTGACACCAGCAAAACAGACATACTGATCCTTCGTCAAATCATGGCTCTTCAGATGATGACCAGCAAGATGA
 AGAATGCATACAATGGGAACGACGTGGACTCTTGTATATCAGTGATGAAAGTAGTGGAAGGAAGTGGAAAGT
 GGCTGTGAGTATCAGCAGTGGCCTTCAGAGTTTGACTACAAATGCCACTGACCATGCTGGGAAGAGTCCAATGA
 GAAAGCCGACAGTGTGGTGTCCGCTCTGGGGCAGAGGCTACCTCCTCACTGTCTTCTGATCTTGTTCCTGG
 TTAGCAGAGAGAGTGGAGATTAATCTCAAACCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCCACGATT
 ATCACTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAAAGTGTGACTTTGTTTCTCATTCAGTTTGGGAGGAAAAGGAGCTGTGCATTGAGTTGGT
 TCTGCTCCCCCAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCTATATTTGTTTGTATGTTTTTCTCATTTGTTTGTGGGTTTTTTTCCAACTGTGATCT
 CGCCTGTGTTCTTCAAGCAACAGGGTCCCTCTTGGCAGTAACATGACGTATTTCTGAAATATTAATA
 GCCTGACAGAAGCAGGTTTTATTATCATGTATCTTATTAAGAAAAAGGCCCAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPO
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKCLKQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCG**ATG**AAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTT**GTAG**GAGCTCTGAGCGCCCACTCTTCCAATTAACATTCCTAGCCAAGAA
GACAGTGAGCACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGCTCTC
TCTAGTGCTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCTAGCTAGTGTCAATTAACCTTAAATGC
AATCAGGAAAGTAGCAACAGAAAGTCAATAAATATTTTTAATGTCAAAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
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[illegible]

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FIGURE 101

MAVLVLRLTVVLGLLVLFLTCYADDKPKDKPDDSGKDKPDFPKFLSLLGTEIIEHAVE
FILRSMRSTGFMEFDDNEGKHSSK

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MAVLVLRLTVVLGLLVLFLTCYADDKPKDKPDDSGKDKPDFPKFLSLLGTEIIEHAVE
FILRSMRSTGFMEFDDNEGKHSSK

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGTCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTGTGCTCTGTGCAGAGCCCAAGGAAGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACTTCTTCTCTGAGCTGGGGGACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLQLLVLLLTPLHLMLLLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELF SQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSM DVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSF P
SSKALICSFP SLQLEQATHQPIY LPLRGT

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FIGURE 104

GTGGGATTATTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTATATGACAGAAGAAAAAGATGCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTACAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGCCATTGCAGCTATAAACAGCATTACGACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTGACCCTAAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTACGCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAACCTGACGGAATGGAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACACACCTCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCAACAGGCAAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAATTTGAAGTGAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCCTACCAAGTGTTCCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTACAGTAGCTGGTACAGA
 TAATTCAAACCTGCTGTTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAATAAACTT
 ACATTTTTT

MSFRKVNIIILVLAVLFLVLVHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVVIAASEDRLGGAIAAINSTQHNRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRVIRGAGNYIYIGYLDYKKERIRKLSMKASTCSFNPQFVFA
NLTEWKRONITNQLEKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQSHITDPMWNVRLHS
SAGRYSQPQVKAACKLHWNHGLKWPGRTSYITVDWEKWIYIDPTGKFNLIRRYEISNIK

FIGURE 106

TGGTTTTTGCCCATAAATTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTAC
TAAAGTTGTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGCGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCCCAGCGTGCAGGGAAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCTGCAGTAAGGGCGGCCGCGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACGAGGGGTGTCTCTGAGCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTCAGGAATTGTAG
 GGCTCAACCTATAGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCATTGCAGCTATAA
 ACAGCATTCAAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGTCCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCCCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAAGGAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
 CTGACGGAATGGAAACGACAGAATATAACTAACCACCTGAAAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCAGT
 GCTGGAACACGATATTCACCTCAGTTTGTAAAGGTGCCAAGTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
 GACCAACAGGCAAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAATTTGAAGTGTAAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAAATCAAACCTGCTGTTGGTTTTAATTTT
 GTAACCTGTGCCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTCTGCCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCCCTGGTCCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
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FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTTTGCATCTGTGTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA
 TCATGTCGGGAAGAGATACAATCCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGTTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTA
 TCCACAGGCATCAGGCAGTGTCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGTCTCCCTTCTGCTGTCTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCCCTCTGGGTGGCTGTGCTGTG
 AGCCTGGGAACGTCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGAATATAAGCCCTT
 TTCGGGCATTGGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGGCTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTCTCAACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACGCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGCCAAGAAGTCAAGTCACTTTACATCTATTAAGTGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACCTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAATTAACAATGAAGGACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATAGATATACCAATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCCTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCCCTATTCTTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGGAAPQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNLKTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAEE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVCDTDLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKBEISDTRIGAVQYTYEQRLEFGFDKYSSKPDIL
LNAIKRVGYWSGGTSTGAAINFALQFLFKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAAGTGGTTGCGAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCCTCCTGTGCGCGCTGCTGCCCTCAGCACCATGGT
 GCGCCAGGTCCCAGACGGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCTCTCCTGAGAATGGCTGAGGAGCGGGCCGAAAACCTCC
 TCCAGCCTTTCCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTACAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCGAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCCTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCAGTCCTTGAGGGCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCAGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCTTCTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAAACCACTTCATCCACAACATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGAGTGCATCCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTCACCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGAGCAGGTG
 GAAATTTAGAAAAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
 AGACTCCTCA**TAA**CCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

MPFRLLIPLGLLCALLPQHGHGAPGPDGSAAPDAHYSFSLTLIDALDITLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQPTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFVEFATLSSTLGDVPFEDVARVALM
RLWESRSIDIGLVGNHIDVLTGKWWAQDAGIGAGVDSYFEYLKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVQSLEAYWPGQLSIGDIDNAMRTFLNYT VWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLRATGDPTLLELRDAVESIEKISKVECG
FATIKDLRDHKLDRMSEFFLAETVKYLYLLFDPTNFIHNNGSTFDVAPITYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEQVEVDELMREFSYLLKRSRKFQKNTVSSSGWPEPPARPQT
LSPENHDORARERKPAKOKVLLSCSPQPTSKALLGQGVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTACAAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTGTATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGAATACCAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGTAGTGTGATGTCATGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTT
 CTTGTGGCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTG
 GGGTATTTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCATGTTGCTCTGGAATAAGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGCTGG
 TGGTCTCCAGACACCTTGAAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCAGGGCCTGGAT
 CTCATAGGTTTTGCGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATACACACGTACACATAAA
 TACACCCAGCACTTGAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTACAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 GTTGAGTTCACCTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTGTTGTGCTCCTTTTTC
 TGTGGTAAAGTACAGAATTGAGCAATAAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSPVIAIGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLVRATLGSQTSAAW
SILKHPPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVEVQGEAIPVLVLAFAFVGFMILIV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

TCCTGCTGATGCACATCTGGGTTTGCCAAAAGGAGGTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAAGTGAAGTCTACCAAAATGCGAGCTTTCACAAATGGTCTAGAGAAGAACTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCAATTGATTCATGTTTGTCTACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGTCTACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCNCAGTTTGAGTTCCTTGTGGCCTANTGAGGAGGGGCCACCCCTTCGCGCGCAAGGCG
GTTNGCAGACCCCTTGCGGCGCTGGGGTATCTCTCGAAGAAAGAGAGGCCCAATACACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAAGTGGCGCTGGGTGTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCAGCGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCCTGCGCGCAGCAGGAGCACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGC GGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCCAACCTGTGTCAGTGGAGGAGTACAGCCCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTATTAAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTACTCTTATGCCATTGGTCCCATCTTCTGTGGGGGAA
 AAATCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAG
 AGCTCTTGACAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTCATATAAACCAAAAAATACTTGTATCAAT
 AAAAAGCTGCATCCACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCACGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 120

MVAATVAAAWLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGGCC**ATG**GCTGTCTACGTGGGATGCTGCGCTGGGAGAGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCGGAGCGCCCTCTCTCGGAGTTGCGAGGAAGCGAGGTGCGAGGTGCGAGGTCTCCGCTTCTCACTGATTTCCAGAGAGGTGGATCGCATGGTCTCCACGCCCATCGGAGGCTCAGCTACGTTCAAGGGTGCAACAAAAGCATCTTACACGACAAGATGTGGGCGAGTGCCCTGGAGACACAGAGGTCCTCCAGAAGCATGAGGCTTTGTGTCCTCCATGAAGACGTCAGGTTGACCTTTGCCAACTCAAGGAGAGGTGGACAAAGCTGCTTCTGGCCTCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGA

CTAACTCCTATGCATGGGTGCTCATCGAGTTGGCCACCGCCAGCGGGCATCATTTCTGGTGCTGTGAACCCAGCCTACAGCCTATGGAATCGAGTATGTCTCAAGAAGTGGGCTGCAAGGCCCTTGTGTTCCCAAGCAATCAAGACCCAGCAATACTACAAGCTCTTGAAAGCATGCTCCAGAAGTGGAAATGCCAGCCAGGGCCTTGAAGATCAGAGCTCCGAGTCAACACATCGACACATCGTCTCGTGGATGCCCTTTGCCGGGGACCTTGCTCCTGGATGAAGTGGTGGCGCTGGGACGACACGGCAGCATCTGGACAGGCTCAATACAAACAGCAGTCTGTCTGCCATGACCCCTACAATCTCAAGTTACCTCGGGGACAACAGGCACCCCAAGGGGGCCACCTCTCCCACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCTGAAACTGGATGAGAAGACACGAGCAGTGTGCGGATGATCCTGCCAACCCCTCGTACCATTTGCTTGGTTCGGTGGGAGCAGCAATGATGTGTGATGTACGTGCACCTCATCCTGGCCTTCCCATCTTCAATGGCAAGAAGGCATGGAAGGCCATCAGCAGAGAGAGAGGACCTTCTGTATGGTACCCCGACGATGTTCGTGGACATTGTGAACACCGACAGACTCTCAGGCTATGACATCTGCACATGTGTGGAGGTTCTATGCTGGTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAGATAAATATGAAGGACCTGTGGTGTGCTTATGGAACACAGAGAAGTCAGCTCCGTGACATCTCGGCACCTTCTTGAGGACATGTGGAGCAGAAGGACGAGAAGCTGGCAGAAATATGCTCACACGAGGCCGGGATCATGAACATGGAGGCGAGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGCTATGCGCTCATGCTGGGCTATGGGTGAGCCTCAGAGAAGAGAGGAAGAGTGGATCAGGACAAGTGGTATGGACAGGAGATGTGCCCAATGAATGACGAGGCTTCTGCAAGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGTTGGTGACAACATCTAACCCGACAGCTCGAGGACTCTTTCACACACACCCGAGGTCAGAGGTGCAGGAAGTGCAGGTTGGTGGGATGAAGACGATCGGATGGGGGAGAAGATTTGTGCTGCAATTCGCTGAAGGACGGGAGGAGACACGGTGGAGGAGATAAAGCTTCTGCAAAAGGAAGATCTCTCACTTCAAGATCCGAAGTACATCTGTGTTGTCAACAACATACCCCTCACCATTTCAGGAAGATCCAGAATCAAACTCTCAGACGAGATGGAACGACATTAATCTG**TGA**ATTAAGCAGCAGGCTGTCTCTGGCCGTTGGCTTGACTCTCCTGTCAGATGAACATGCAACTGGCTTTAGTGCACCTAGATGTCCCCAGCACCGGTTCTTGAGCCAGGCACATCAATGTCAAGGAATTTGACTGACCAACTAAGAGCTCTGGATGGGTGCGGAACTCGCTTGGGCACAAGGTGCCAAAAGGCAGGCAGCTGCCAGGCCCTCCCTCTGTCCTATCCCCACATCTCCCTTGCTGTCTTGATTTGGCATAAAGAGCTCTGTGTTTCTTTGAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEV DKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKV GCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNI VNNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLV VAYGTTENSPVTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGE PQKTEEAVDQDKWYWTGDVAT
MNEQGFCIKIVGRSKDMIIRGENIYPAELEDF FHTHPKVQEVQVVGKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKI QKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTCACGGGC
 TTCTGGCGTTTATCCAGCTGCAGCAATGCGCTCAGGATCGTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGTCATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCGCGGCTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA
 GCTAATGTGACTGTGTTCCTTGCCGTGTCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTACAGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC
 CGCAGCAATTGAGGGCAGTATCTTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCCTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCCTGTTCCCAACCATGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTGTCTC
 TCCGCTTGCTCCTTGTGTATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGTGGGACAATGGCTCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCCATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSApVRPTSTTKPMPAPTSQTPRQGVHEASRDEEPRLTGGAAGHQDRSNG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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[illegible]

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTVEVQPSGGSLWNLRRLLEPLDANVDA

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FIGURE 128

AAACTTGACGCCATGAAAGATCCCGGTCCTTCTCGCGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCTCTGAGGAAGAAAGCACCATTTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCTTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

[illegible]

FIGURE 129

MKIPVLPAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
 FLNWHALFESIKRKLPLFLNWDAFPKLKGLRSATPDAQ

FIGURE 130

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTCC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCC AAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCATAATTAATTGTAACGATTAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTGTAGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGGCTCTG
 GCTGCTGTTGTTCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAAATTAT
 CCTACAGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGACGAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTGTCTCGGAAAAACCCAAACTTGTGATGCGAATACACCAAAAAC
 CAGGCTCGGAAATCTATGAAAGATACCTTAGGAAAGCCAGTCTGCTAAGGATGTCCATCTGT
 GGATCACTGCAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTGTGTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTACAAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAATGTTGAAAACGAAC**TAG**TAGTCATCATAGGACCATAGTCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTCTTAAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

MEWVASSPLRLWLLL LLLPSAQGRQKESGSKWKVFI DQINRSLENYEFCSQNCSCYHGVE
EDLTFFRGGISRKMMAEVVRKLGTHYQITKNRLYRENDCMFSPSRCSGVEHFIFILEVIGRIPD
MEMVINVRDYPQVPKWMPEAIPVFSFSKSTSEYHIDIMYPAWTFWEGGPAVWPIPYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTPERDPLILSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDCKYKYLFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDDVAQEIAERGSQFIRNHLQMDDITSEYWNLLSEYSKFLSY
NVTRRKGYDOIIPKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCC**ATG**GCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTGCAGCTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
 TCCTCTGCTTTGTGCTCCATGTATCTCCTGGCTCCTCATCTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGCCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCCCTTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAATCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCTCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATCTGAGTTTCAGCCA
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCCCTCACCACCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAGTCAGCCTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEFWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLLLTYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTCTAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAACCCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTCTG
 AGCTGCTGTGGATGCGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGCTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATATTGGC
 ATTCAGGTGGGTAAGTGTGTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACCTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT
 TCTTTACAGAGATTTGTTGCCAAGGATCTATGAAATCATGAGTGGGTTGGGTTATATAA
 TGTCAGAGATTTGGTGCCCAAGGATCTATGAAATCATGAGTGGGTTGGGTTGGGTTATATAA
 GAAGATGTTTATGTGCGGATCTGTTTGAATTTATTAAGTGAACATTATATTCCAGAAGA
 CACAAATCTTTCTTCTATATAGAATCCATTTGGATGTCTGTCACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCAAGGAGATCATCACTTTTTTGGCAGGTGATGCTAAGGAACACC
 ACATGCCATTATTTAACTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAATTTATGGGAGGTGAGTGTGCTGGCTTCACTG
 AACTGAACTCATGAAAACCCAGACTGGAGACTGGAGGTTTACACTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACCTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTAAATTA
 CTTCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATCTTTTACATGCAACATTTTCCAGTTACITAACTGATCATGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTCAATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAAATTAAGCAAGAAAATCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLGGQAEK
EDKMLALSLEDEHLLYGDIIRQDFLDYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPYPCSLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACCGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYININVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
 IWDYNGFAATRLFQKKTCIVHKMNKEVMPISIQSLDALVKEKKLGKGPGGPPPKGLMYSVN
 PNKVDLDSKFGKNIANMCRGIPTYMAEEMOEASLFFYSGTCTTSVLWIVDISFCGDVTEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTTCGTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCTAGTATTAAATTCCTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT
 TTGTTGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAAAGCAAAGGGA
 TTGAATCCGGATGGAACCTCCAGCCCTTTCAACCCCTGGGTGGATTTTCTCCAGCCCTCAAGCC
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTCTTCTTTGAGCCTGCATCAGTTCCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAAACGAACTGATTAGGATTGATTCTCTGAAACCCCTCTA
 GGTCTCTAGAACTGAGGACAGTTTCTTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTAAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTTCTAAAAA AAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETIRLY
TRKKPNYELLEKEVEKRVKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKRSRSQ
SKSRDHSDAAKKRHERGHHDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTATCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTTTGTTCATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTGATTTCACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACITCA
GATTCGGTTGCCAACINGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACCTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTACTG
GAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGAAGCAAAGGGATT
GAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTCCTCC

FIGURE 143

GGCACGAGGCCCTCGTGCCAAGCTTGGCACGAGGGTGACCCGCGTTCTCGCACGCGTC**ATG**GC
 GGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCACAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGACCTCTTCACAGAGGCCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGTTGCG
 GGAGGAGACCCTCGAGCTGGGCCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCAGGCCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTCGGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACCAGCTTCTGTCTCCCTGTTTCATCTGTGGCTCTGGACAAAGCCCATGACGGGAC
 TTCTGCAACAGCCGCGGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTTCGA
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGCTGCGCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCCTACCTGTGCTTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCCCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
 GGACGGCTGCCGTGCCAGCTGCTGCGCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GGCGTTCCCTTCACCAAGTGCCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCGCTCA
 GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVLTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGERSVCLTFAFLFLLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWWDALPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLHLSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSILQYLTPLIILTNLCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAS

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FIGURE 145

CGTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

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FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACTGGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGG
 CGCTTCTGTGCTGGCTTGGCTTGGCTCAGTCTCTGCTAACTACATTGACAATGTGGGCACCTGCACCTTCTGT
 TATTGAGAACTCTGTAAAGGTGCTCCCACTACGGCCGTGACCAAGATAGGAAGAGGGCTCACAAGATGGCTG
 TCCAGACGGCTGTGGAGCCTCAGACCCAGGGCTCCCTCCCCAGAGGTTTCTGAGCTGCCACCACTCTCCTTAA
 TGACAGACGAGCCTGGCCTGACACAACCTGGCTACGTGTCTCGCAGAGGACGGCCAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAAGTGGGCAAGGCGGCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAATAAATCGAGCTTTGAGTGTTCTTCCAAGGACAAAGAGCGGAGTGCAGTTGCCAACCATGCCGACAGG
 GCAGGGAAAAATCTGAAAAACCCACTGCCCTGAAGTCTTTCCAAGGTTGTACCACTGATTCAGATGGTGAA
 ATTACAGCATCAAGATCAATCAGTAGATCCCAGTGAAAGGCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTTATCCAAACACATTTATCGTGATGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTCAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACACAGCTGTGGCTCTCTGCCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGACAGGAACAAATGGACAGGCC
 GGATGCCACAGACCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCGGAGGAGCAGCTTGGAA
 TAAAACCTGGTGGCAGGTTGGATGAGCCTGGGGTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAG
 TGGCGCTCATCTGATTACGGCCAGTGAAGACGTGTTCACTCTGCTGTCGCCCGAGGTTCGCGAGCGGAGCC
 CTGACATCTTTACGGAAGCCGGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACT
 CCCAAGCCCTCCATCCTACAATTACTTTGTATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGACGGGGGAGCATCACATAGAGAAATGGGATTGCGCTATCTATGTATCAGTGTGGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGATAAAAAACAGGTGACATTTGTGAATGTGGATGGGGTCCGAAGTGA
 GAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT
 CAAAAGATGATGAGCCCGAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAAACCAACATGGCCCAACCCA
 GTGACTGGTCCCATCTGGGTGATGTGGCTGGAATTACCACGCTGCTGTATAACTGTAAGATATTTGATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCAATGTAGGAGGTATGAAGAATACAATGGAAACAAACCTTT
 TTTTCATCAATCCATTGTTGAAGGAACACGAGCTACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTG
 CTGTCATGGTGAAGTACATCAGGAATGATACATGCTTGTCTGGCAAGACTGCTGAAGAACTTAAAGGAAGA
 ATTACTCTAAGTATTTCTTGGCTGGCACTTTTATAGAAATCAATGATGGGTGAGAGGAAACAGAAAAA
 TCACAAATAGGCTAAGAGTTGAACACTATATTTATCTACTACACATTTTATATTTTAAAGAAAGATACATTGT
 AAAAATGTCAAGAAAGTATGATCACTAATGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAATTA
 AAACACTAGTATTTTTCAGTGTGGAGGATTTCTATTACTCTACACATTTTATATTTTCTATTCAAT
 AAAAGCCCTAAACAACTAAATGATGATTTGTATACCCCACTGAAGCTGATTAAATTTAAATTT
 GGTATATCTGAAGTCTGCCAAGGTACATTTAGCCATTTTAAATTTAGCACTAAATATTTTAAATGCA
 TTGCTGAGAAACCTGCTTTCATCAACAGAATAAATATTTTTCAGAACTTAA

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAP EVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQH IYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLR
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLG IKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHD LRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDIFQEAGWNSNGSWS PGP GERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNV DVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPP SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPF FIKSIVEGTPAYNDGRIRC GDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAAACATCATCAGCCCAGCAACAATGGTGGC
AATGTTCAAGGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTGAATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCCGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTTCATGTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAAATATAAATGCTGTATTTATA

FIGURE 150

GGCACGAGCCAGGAAGTCTGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGGAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
AGCCAGACATCGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCTGGAGA
GCCCCATCCTTGCCCTGCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTGAGGAGCGCAAAGCAGCAGCCATG**TAG**AATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCCTGTTCTGATTGGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALPLRYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184



FIGURE 152

GGTCCTTAATGGCGAGCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTGAGTGGAGAATTACACACCAAGGAACCCCTCACCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
TTCGATGGGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACTCAGGGCCAC
AGCCACCACCCTCATCCTTTGTGTCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCCTTTAGAGTGACAGGTAAAGCTGATACAAAAGGCTCCTGTGAGCAG
GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCAGTGCCTTGATTCTT
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
AATTTTAAATTATTTAATAAGAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCTCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCQVGGQVDEKTFLL
HYDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81



GGGAAAGCCATTTCGAAAACCCATCTATACAACTATATATTTTCATTCTGCTGCTAGCTG
CCTTGGGCCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGGAATGGAG
TTGATCCCAACCATAACATCGTGAGGGTTTAAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTCTTTGCAGAGGATTCCACCTTCAAATCATGAACCTCGGCCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
CCTCTCTCCATCAAGCATCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCTTTTCAATTAACCTGTATTTTCAATTTTGAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGPTEQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAG
 CTCTTGTCAGGTAAGTGTGCACCACCACCTGGAAATGCCATCCTGCTCCCGTTCTGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGGCCCC
 AGAACTGCCCCCTCCGTTTTGCTCGTGCAATAACCAAGTTCAGCAAGGTGGTGTGCAGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAAACTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGGCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCCCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTGATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTTGTGGAAC
 CAACTTGCCCCACAATAACCTCTCTTTTGCCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCCTACCTCGTGAGGTGGACCAGGCCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACCTTAAGTGT
 CGGACTCCCCCTATGTCCCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCCAAGGATCTCTGTCTTCAACGACGGCACCTTGAACCTTTTCCACGTGCTGC
 TTTCAGACACTGGGGGTACACATGTCATGGTGACCAATGTTGAGGCAACTCCAACGCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAAACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTCAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCCACCAGCAGCGGAGTACAGTC
 ACAGCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCG
 AGCAGCAACAGCAGTCCGTCCGGTGATCAGGTGAGGGGCGAGTAGTGCTGCCCAACATTC
 ATGACCATATTACACTACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTGTGACCCACAGTCACCACTATCTGTAACCTTATATAATTAGACCCCA
 TACCAGGACAAGGTACAGGAACTCAAATATGATCCCCCTCCCCAAAAAACTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAGCTTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA
 CAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSNQSFKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRDLGELKKLEY
ISEGAFEGFLNLKYLNLGMCNIKDMPNLTPLVGLEELEMNGHFPFIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDHLFTPLRYLVELHLHHPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTVNAGNSN
ASAYLNVSTAEINTSNYSFFTIVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDITDKMQTSLDEVMTTKIIIGCFVAVTLAAAMLIVFYKLKRHHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

CGCTCGGGCACCAGCCGCGGAAGG**A**tgGAGCTGGGTGCTGGACGCAGTTGGGGCTCACITTTCTTCAGCTCC
 TTCTCATCTCGTCTTGGCAAGAGAGTACAGTCATTAAATGAAGCTGCCCTGGAGCAGAGTGGAAATATCATG
 TGTGCGGAGTGCTGTGAATATGATCAGATTGAGTGGCTCTGCCCGGAAGAGGGAAGTCTGGGGTTATACCAT
 CCGTTGCTGCAGGAATGAGGAGAAATGAGTGTGACTCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAAC
 GCAAGAGCTCCGGAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAG
 TGCCGAGCAGCTGATCGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCGCAAGGGGTGAGATTTT
 GTTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACATTATGCTAAAGCTGGGTTTGTCAATCCAATTA
 GATTTGTCTAGTTGAGTCTGGAGTTTGAATACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAAC
 CGCGATGGCCAGATCATCAAGCTGTCTGTGGCAACGAGCGGCAGCTCCTATCCAGAGCATAGGATCTCTCACT
 CCACGCTCTCTCCACTCCGATGGCTCCAAGAATTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT
 CCTCTCATCTCCCTTCTTCCATGACGGCAGTCCGCTCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTTG
 GCAGGCTATACTGGGACGCGTGTGAANAATCTCCTTGAGAAGAAAGTCTGTCAGACCTCGGGGGCCAGTCAA
 TGGGTACCCAGAAAATAACAGGGGGCCCTGGGCTTATCAACGAGCGCATGCTAAAATTGGCACCGTGGTGCTT
 TCTTTTGAACAACTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGGCAGCAGAAATGAGAGTGGTCAGG
 AAACAGCCCATCTGCATAAAGCCTGCCGAGAACCAAGATTTCAGACCTTGGTGAAGAGAGACTTCTCCCAT
 GCAGGTTTCAGTCAAGGGAGACACCATTAACAGGCTATATCAAGCGGCTTCAAGAGCAGAACTGCAGAGTG
 CCGCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAATCTGCATACCCAGCTCCAG
 TATGAGTGCATCTCACCTTCTACCGCCGCTGGGAGCAGCAGGAGGACATGCTGAGGACTGGGAAGTGGAG
 TGGGCGGGCACCATCTGCATCCTATCTGCGGGAAATTTGAGAATCATCTGCTCCAAAGACCCAGGGTGGC
 GCTGCGGCTGGCAGGCAGCATCTACAGGAGGACGCGGGTGCATGACGGGAGCCTACACAGGAGCGTGG
 TTCTAGTCTGACGCGGTGCCCTGGTGAATGAGCGCATGTGGTGGTGGCTGCCACTGTGTACTGACCTGGG
 GAAGGTCAACATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGAAATTTACCGGGATGATGACCGGGAT
 AGAAGACCATCCAGAGCTACAGATTTCTGCTATCATTTCTGCATCCCAACTATGAGCCCATCTGCTGTATGCT
 GACATCGCCATCTGAAGCTCTTAGACAAGGCCGCTATCAGCACCCGAGTCCAGGCCATCTGCTGCTGCTGCCAG
 TCGGATCTCAGCACTTCTCTCCAGAGTCCCAATCATCTGTGGCTGGCTGGAATGCTGCTGGCAGACGTGAGGA
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCAAGTGTGGTGAATCGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGTGAGTGTCACTGATAAATGTTCTGTGCGAGCTGGGAACCCACTGCCCTTCT
 TGATATCTGCACTGCAGAGACAGAGGCGATCGCGCTGTGTCTTCCCGGGAGCAGCATCTCCTGAGCCAGCT
 GGCATCTGATGGGAGTGTGAGCTGAGGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCTTCAACAAG
 GTGCTGCCTTTAAAGACTGGATTGAAGAATATGAAAT**G**GAACCATGCTCATGCACTCCTTGAGAAGTGTTTC
 TGTATATCCGTCTGTACGTGTGTCATTGCTGGAAGCAGTGTGGGCTGAAGTGTGATTGGGCTGTGAAGTGG
 CTGTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTACCTCCATTGCTGGTGAAGTGT
 GCGCGCTCCACTACTAGGACAGCCAAATGGAAGATGCCAGGGCTTGAAGAAGTAAGTTTCTTCAAGAAGACC
 ATATACAAAACCTTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTG
 ACCAGGGAAGATCTGGGCTTCAAGAGGCCCTTTTGAAGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCC
 CAGGGCAGCAGCTGGGATGTGGTGCATGCTTTGTACATGCCACAGTACAGCTGTGGTCTTTCTTCTTCC
 CCATCTCTTGTACACATTTTAAATAAATAAGGGTTGGCTTCTGAACACAAAAA
 AA
 AA

MELGCWTQLGLTFLQQLLISSLPREYTVINEACPGAENINIMCRECEYDQIEVCVPGKREV
 GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
 CMRCGQVLRAPKQQLLESYPLNAHCWTIHAKPGFVIQLRFVMSLSEFDYMCQYDYVEVRD
 GDNRDGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEETACSSSPCFHDG
 TCVLDKAGSYKCACLAGYTGRQCNLLEERNCSDFGGPVNGYQKITGGPGLINGRHAKIGTV
 VSFFCNNSYVLSGNEKRCTCQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPH
 QLYSAAFQKQLQSAPTKKPPALPFGDLPMPGYQLHHTQLQYECISPFYRRLGSSRRTRCLRTGK
 WSGRAPSCIPICGKIENITAPKTQGLRWPPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
 RTVVVAACHVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
 ADIAILKLLDKARISTRVQPICLAASRDLMFSTQFESHITVAGWNVLADVRSPFGKNDLTRSG
 VVSVVDLSLCEEQHEDHGIPIVSVTDNMLCSAWEPTAPSDICTAETGGIAAVSPFGRASPEPR
 WHIMGLVLSWSYDKTCHSRSLSTAFTKVLFPKFDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACTGACTTTCCACCTTTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACACTTCGTGGGTGCCATTCAAGAGATTCCATAAAG
 CAAAGGAGTTTATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCTACCCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTCAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGTTGAGCTCCAAAG
 AATGAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCGAAGCAGATGAAGCTTTACACCAAGTGTACGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTGGTGCAATGACCCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTGAATCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCAATTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGTTGCAAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAA
 TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLTFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLI FKPDLTLEEVAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALESREQFFKVNG
FSNNYWGWWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRDGLSSCSYKLVSVEHNPLYINITVDWFVGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCCGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCTCCGCGTCCGCCACGCTTCTCCGCTCCGGGGCCCGCA**ATG**
 GCCCAGGCAGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCTGCTCTGCCCTGGGG
 CCGGCGAGGGGTGGCCGCGAGGCCCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA
 CGGGAGCCGTTGGTGACCATCTCGGCCAGCCTGGTGGCCAGGACCAAGCGAGCCTGGCCCTG
 CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGCGAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCCGCCAGCTGCCCGGGGAATTCCCGG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCCCTCCCCATCACAGAGTTCCCTCGTGGGGGACCTTGTTGTCAACCAGAACACTTCCCTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCTCTGAAAGTCTCCTTCTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCCTTGTCTCTCAGAGCTGGGACTTGGGGAGCGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCATCATCGGGACCTTACCGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAACCCCTTCGAGGCATCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGAACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTCTGGCGTCTCAAGCCTGAGTGCCCTCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCTACAACCTGACCCACACCTTCAGGGACCTTGGGAGTAC
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA
 TGTGGCCTTCATCATGTACATGACCCCTGCGGAATGCCACTCAGCAAAAAGGACATGGCTGGAG
 AACC CGGAGCCACCTCTGGGGTCAAGTGTGTGTGCCAGATGTGCTGTGGGCCCTTTCTGTGT
 GGAGACTCCACTGAGTACCTGGAAATTGTTCTGTGAGAACCCAGGGCTGTCTCCGCCCTCT
 ATAAGTCTGTCAAAACTTACACCGT**TGA**GCACTCCCCCTCCCCACCCCATCTCAGTGTAA
 CTGACTGTCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAAT
 TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTCAAGCCACTGCCACAAGCC
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCGAGACT
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCCTGGCTGCCACTGCCCATTCCT
 CTCATATTGGCACATCTGTGTCCATTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAAGGTCATAAAGGTTAAAAATCCATTAACATAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA
 CACACACACAGAAATATAAACACATGCGTCACATGGGCATTTCAGATGATCAGCTCTGTA
 TCTCGTTAAGTCGGTTGCTGGGATGACCCCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCACTTCTTGC
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACTGAGTGATTGCGAGAGTGCTTTATAAATATCACCTTATTTTTCGAAACCCATCTGTG
 AAACCTTCACTGAGGAAAAGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCCGGGCCGG
 TGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCGAGCGGGTGGATCAGGATCAGGA
 GATCGAGACCACCTTGCTAACACGGTGAAACCCGCTCTCTACTAAAAAAATACAAAAAGTT
 AGCCGGGCGTGTGTGGGTGCTGTAGTCCAGCTACTCGGAGGGCTGAGGCAGGAGAATG
 GTGCGAACC CGGAGCCGAGCTTGCACTGAGCCAGAGTGGGCCCATGCACTCGAGCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTTQNTSLPWPSYLTKTVLKVSFLLHDPNFKLTALFLYSWDFDGTQ
MVTEDSVVYYNYSIIGTFTVKLVVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCKT

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FIGURE 166

CTGTGAGGAAGGACCATCTGAAGGCTGCAATTGTCTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACCATGTTCCTGTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
 AGTCTCCTTTGGTATCCGAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAAATGGAGCGAGGAGCCAAAGGAGAAGAACCACAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAGGATCCCACCTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGAACCTGTCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGGTAGGAGTGTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACCTTGCCAAAT
 GGGAGGTTTAAAGAACTCATGAGTAAACATGTTCACTTAATGTGTACC GGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGGCCATGGTGAAGGCTG
 CCCACACGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACATGA
 CTGAACATGTGCAAGATAAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGAAGTTTTGAAATTTGGAGCCACAGTTTACCC
 TGTTGCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGACGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACAC
 AAGGACAGGAGCGCTCTCCTGAGCCTGCCCTCCAGCTGGCTGGGGCCACCGTGC GGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACTGCTGTGTCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCAGAGCCGACGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTTTCTTTTACAATAAGTCTGTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTGGGGAGATGTGGCCATGCTCTTGTGTGATAGAT
 GGGCGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGATGTGCTGGGGCGGCCACCCG
 CTCTCCAGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCCTCAACATCGCCCCCAGC
 CTTGGAGCTCTCAGACATGATAGGAAGGAAACTGTCATCTGCAGGGGCTTTTCAGCAAAATG
 AAGGTTAGATTTTTTATGTTCTGCTGATGGGTTACTAAAGGAGGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGAGAACGTGTGTTCTGACTCCAGGCTAACCTGAACTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGATTTCTACCTCACAGGCTGTTGTGGGATTAAGTGTCTGCGGGTGAGTGA
 AGGACACATCAGGTTAGTGTTCAGTACAGGCCACAAAACGGGGCAGCGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTCTTGTGTGAGTAAATAAACTGGCTGGTGA
 TGA

FIGURE 167

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIVPAIFGVSF GIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAEELESWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLPLRLAFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRP RNGGICVANH
TSPIDV IILASDGY YAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVM MFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMTSWAIVCSVWYLP PMTREADED AVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

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FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGG**GATG**CGCTGGCGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCAGGCTGTTCACCATCCTGCCCCGGGCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTAAGGGAGTTGAATCAGGCCGTGCGGACGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTTGGGGAGAAGAGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCC**TGA**AAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

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FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACCATAACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTCGCCAGGAACCCCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCCTCTGTGTCTCCTGTGGTGCCCTT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAACTCCTAACATATGCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAAATCCCCACTCAC
TGCTCAGATGCCAGACACCAAGGCTATTTGCCTATGAGAAATGTTATCTTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTHEYDTIPHNTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTCTCAGCAGAAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAA
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAACTCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATAACCGAAAA
AGATGGAATAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAAGAGATGAAGAGTGTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCATATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCTTGACAAT
TTTTCATGAAATTATTCCTCTTCTGTTCATAAATGATTACCCTTGACCTTAA

FIGURE 174

MKMLLLCLGLTLCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTT
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCACTGGTGGTTTTCATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTTGGGTCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAA

FIGURE 176

MTCCEGWTS CNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHL
IHFSVFLGLLL VGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTGGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAATCACTTGCCCTGC

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC
GAACTGTGAC**ATCG**GAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCT**TGAG**CACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCTCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCCCTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCTCA

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
TGGCTGGGCGCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCCGCATCTTGGCTTGGACCTATGCCTTCTATAACAACTGCCGCGGGCTCC
AGTGTTCACAGCCCCCAAACGGAACGTGTTTTGGGGTCACTGGGCTGATCATTCT
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGT
ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATTCCGGTCTATCA
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCCTGAAGCCCTGG
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCTCGGATGCTGAC
GCCCGCCTTCCATTTCACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGC AAAA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCTGCTGGACATGTTTAG
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGTCTTGACAGCCATTG
TCAGGAGAGGCCCATGAATATATTGGCCACCATCTGGAGCTCAGTGCCTTGTAGAGAAAA
GAAGCCAGCATATCTCTCAGCAGCATGGACTTCTGTATTACCTCTCCCATGACGGGCGGGC
TTCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTCTCCGGAGCGGCTCG
CACCTCTCCCACTCAGGATATTGATGATTTTTTCAAAGCAAAGCCAAGTCCAAGACTTTGG
ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAGGCCAGTGGCCTCTC
CTGGTCTGTACAACTTGCAGAGCAGCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
AAGAGCTTCTGAAGGACCGCATCTCAAAGAGATTGAATGGGACGACTTGGCCAGCTGCC
TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCG
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
TCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
CCCTTCGCTTTGACCCAGAGAAACAGCAAGGGGAGGTCACCTGCTGGCTTTATTCTTTCTC
CGCAGGGCCGAGGAATGCATCGGCAGCGCTTGCCTGAGGATGAAAGTGGTCTCTGG
CTTGATGCTCGGCACCTTCGGTTCTCTGCAGACCACTGAGCCCCGAGGAAAGCTGGAA
TTGATCATGCGCGCCAGGGCGGGCTTTGGCTCGGGGTGGAGCCCTGAATGTAGGCTTGCA
GTGACTTTCTGACCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGP IIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGE GILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQH LASEGS
SR LDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFFKDKAKSKTLD FIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLR LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGLWLRVEPLNVGLQ

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FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAAACCATA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAATAAGCATCTGT
TAGTCAGCTCAGAAACCCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTCAATTGTTACCTGGAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTT TAGTTC CCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCA GTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGAATCGCCCAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAC TGTA

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCCCTGAGCCCCCACGCCCTGGGCCAGAGTCTTT
 GTCCCCGTGTGCGCATGTGTTCAAGGTGAGCCTCTCCAGAAGTGAGATCATGGACAAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTTCTAACAAATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTG
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACCAAGA
 GCCTCCTTGTTTACATAACACAGGTTACCCTACAAACCACTGTCCCCACACACCTTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLDFLGLVHLGQLLI FHIYLSMSP T LSPRSPQGW
V VRAAHL T PLLEYVPNPEPPTPGARV FVPRVRMCSG SASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAE LTPR PAGV VPGA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATAACAACGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCACTCAGCTTCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCCTGCCTGTGGGCTCAAACGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCTTTACATGGCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCAACACCTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGAAGCATAGTAAGAGCTTCAAGGAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTATAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTCGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTGTTTACCCAC
 CCCACATCTCACACATCCAGAATCCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLILLSAILSMLSLSFSTTSLLSNYWFGTQKVPKPLCEKGLAAKCFDMP
VSLDGDINTSTQEVVQYNWETGDDRF5FR5FR5SGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLP5DCQLG5RRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHODGAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGGAGGTGAGCTTTGGCCAGATGTTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTATTCTGTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCCTATTCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCTTCCCCCTGCCCGCCGCTAGATTGAG
GACATTCGCCCTGTGTGCCACCAAACAGGACTTTCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAATGTAGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

FIGURE 193

GTAGCGCGTCTTGGGTCTCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGGCAGGAGCGACGTCA
 CCGCCATGCGAGGCATCAAGAGCTTTGATTAGTTTGTCTCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTT
 GGATGTGCCCTTCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTTTACATCCTTTCACCTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTTGTAAGGAACCTTGCATCTTTTC
 TTACRAACGGGCATTGTCTGTGTCAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGA
 GCTTGTGCACTTCTCTCACAGGAACACAGTCATCTTGGCACTATACCTAGGCTTTTCTGGTCTTGGGAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGAAGAAGTAATCTGAACCTATTGCAATGGACTTCCCTGCTCATTT
 GTTGGCCATTCCGACACAGGAGATGGGSCAGTTAATGCTGAATGGTATTAGCAAGCCTCTTGGGGGTTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGGTGAAGGATTAAGAAGGATTTTCT
 CTTTTGGAAAGGCTTGACTGATTTACACCTTATCTATAGTAGCTTTTGTGGTGTCTGCTGAATTTAATAT
 TTATGTGTTTTTCTGTAGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAAATCCGCCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATTAAT
 TAGCCTCCATTATTACAAAAAATTATAAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAAGTGTTAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA
 AGGTAAAGGTTGTAAGAACATTTTTAGATAAGGTTTTTATTATGTTTATTATGTTAGAGTGAGTTGCAATGT
 GGGGAAGAAATGACATTGAAATTCAGTTTTTGAATCCTGTTCTATTTATAAGTGAATTTTGATCTCCATC
 AACCTTTCTATGTTTTACCTGTTAAATAGGACATACATGGAACCACTACTGATGAGGAGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTCTCTGCTTCCCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATATAGTTAATAACACTTAGAAGTGTTTACTTACCTGGAAAAATTTGCTATGCCGTACATT
 CAGAGTGCCCCCTCCCTGCAAGGCCCTGCCATGATTAACAAGTAACCTTGTAGCTTACAGATAATTCATGCA
 TTAACAGTTTAAGATTAGACCATGGTAATAGTAGTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAACCTGTTTGTATTTGAGTTCATCATGATAGATCTGCTGTTT
 CCTTATAAAGGCATTGTTGTGTGAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATCCCACTAACCAAGGCATGATCAATTTATAGTGGTCTTACATCTAATAATTATCAGGA
 CTTTTTTCAGGAGTGGGTTATAAAAAACATTCAAGTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATG
 TTTATTGAGTTACTTACATAAAAAATTAATTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT
 TTTATGAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTGTTGACGCTTTTACTAAAGATGCCTAA
 AGCCACAGGTTTTATTGCCCTAAGCTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG
 GCGTGTGGCTGGAGCCTCCCACTGGAGGCTGAAAGTGCTTGTGGTATTATAAGTTCAGATTTCAAGAGGAA
 GGTGCAAGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTTGCTTGTGATCTACTGGACCTTT
 TTTTTTCAGGAAGTGCAATCTCTGGTCTCCCTATTCTTCTGATGTCAGTGCAGTGCATGCTGCTACTG
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTTCTATATACATTAATGCAATGGCAGCAT
 GTGCTCTTGAACCTGTATACTAGCTTGACATATGTGCTGCTCTGATTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGAATTCACCTGATACCAACATTACCATTCTCTATGGAAGAAGAACTTTTGATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAAATAA

[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRI FQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTEHLEHNDLVKVNFAHFPRILSLHSLCLRNRNKVAIV
VSSLDWVWNLEKMDLSGNEIYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFFPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTQRRKQKQKQTMHQAAMSAQEYYVDYKPNH
IEGALVIINEYGSCSTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGAATTGACGTGCGAGCCAA
CTGGAGCCAGAACCAGACCCCGTGCGCCGGCGGCGCCGTTGAGTTCCCGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCTCTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCCTGCCGTCTTCGCGGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVRVRSISALGRTFTRDEDLAVFLASR
AGRRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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[illegible]

FIGURE 201

TTGAGCGCAGTGAGCTCCTGCGCGTTCGCGGGCGTTCTCCAGTCACCCCTCCCGCGGTACCCGCGGCGCGC
 CCGAGGGAGTCTCTCCAGACCCCTCCCTCCCGTGTCTCCTCAAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGAGAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAATGACTTCGAAATTTATCTTGGTGTCCTTCATACCTGCTGCACCTGAGTCTTTC
 AACCCCTTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTATGGATTCCGTTGGGATTACT
 TATATAAAGTTCCAAAGCCCATTTTCATTATATATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
 TTTATTAACAAAACCTTACCCTAACCATTTACTTTGGTAAGTGGCCTCTTGCAGAGAAATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTCCGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCGAAGTTT
 GGAAGAAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGTGACGCCATGTGGCCCGGA
 ACAGATGTAAATAATACATAAGCGCTTCTCTACTCATTAATGAGTGTGAGTTCATTGAGAGTAG
 AGTTGCCAAAATTGTTGAATGGTTTACGTCAAAAGAGCCATAAATCTTGGTCTTCTGATTGGGAAGACCTG
 ATGACATGGGCCACCAATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAATTTCAGATATTGACAAAGATT
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGAACACTCTGAACCTAATCATCACAAAGTATCATGG
 AATGACCGAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACAGTACCTGGATAAAGACCACTATACCTGATTG
 ATCAATCTCCAGTAGCAGGCATCTTGGCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAATCTACGCT
 CATCCTAATCTTACTGTTTCAAAAAAGAGACGTTCCAGAAAGGTGGCATTACAATAACAACAGTCGAATTCA
 ACCAATCATAGCAGTGGCTGATGAAGGTGGCAGATTTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAAATTTTTCAGCCATGGTCTGCTTCAGAAAAGATTTC
 TCAAAAGAACCCATGAATCCACAGATTTGACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTCTGGAATGCCAGGATCTGCTCAATTGACGAATGCCAAGGGTGGTCCCTTATACACAGAT
 CTATACTCCTCCTGGTAGTGTTAAACAGCAGAAATGACCAAGAGGGGTCATACCCCTATTTCATAGGGGCT
 TCTCTTGGCAGCATTATAGTGATTGTTTGTAAATTTTCAATTAAGCATTTAATTCACAGTCAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTTATCAAGCCTAATGTTACTTTGAGTGGATTGTCATA
 TTGAAGTGGAGATCCATAAATTATGTCAAGTGTAAAGGTTTCAAAATCTGGGAACCAAGTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACAGGCCAAA
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTATTTGGAAGTGGCCGAGATAATGTATATTTAGCACTTTGCACTATGTAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCTCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGCTTATAAC
 TTGATTGAAAAATGACAACTTTTGACCCCATGTACAGAAATCTTGTACGCAATGTTTCARACTGAAGGAAAT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATTAATGAGAGAAGAAGAGGTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTGGAGATGATTTCCCAACAGCAGAAATGCAACTGTGGGAT
 TCTTGTCTTATTTCTTCCAGAGAACGTGGTTTCATTTATTTTCCCTCAAAAGAGTCAAACTACTGACAG
 ATCTGTCATAAATATGTTTCTGTATATAAATATTGATTTCTGATGAGTCATATTACTGTGATTTCA
 TAATATGAAGACACCATGAATATATCTTCTCTATATAGTTCAGCAATGGCTGAATAGAGCAACCAAGCA
 CCATCTCAGCAATGTTTCTCTGTGTTGTAATTTTGTCTCTTGAATTAATCACTATTATACATTAA
 AATCAATTTGGATAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSLSSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRINKSFSLDHMNIYDSKFWEETPIW
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISIDDKKLGyliQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDKHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCCACGGGCGGGACCTTTGTAAC TGCGGGAGGCCCCAG
 GACAGGCCACCCCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTTGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGA ACTCACAA
 CCAGATCCAGAGGCAACAGGGACATG GCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCCCTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
 CAGCTCCCACAGTTTCAGGT CATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCAC TACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTTCCTTACCACAAAGTTTGAGATCCTGGATGCCCGCTCGTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCTCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTC TGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
 AGATTC AACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTG GACTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCAC TTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCAAGAAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYPKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGLRLKLFSSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVRLSSFTTSLRSWMPV VVVVSFILD
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLKQMNVLAAKIQHLEFS
CSEKPLD

[illegible]

FIGURE 206

MLCLCLYVPVIGEATFEQYFESKGLPAELKSI FKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKLK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTMGW
WRHLVAGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCAGAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAATGTGCCTTGCCACAAAAAAG
 CATGCAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTACACAAGTGTTGTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAAGTACGACCTTCTTTTTAAACAAAAAA
 AA

MASLQGILFWSIISIITIIILAGATALIIGFGISGRHSITVTTTASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHFEKPEKGDELSEQDEMFRGRGTAVFADQVTVGNASRLRKNVQLTD
AGTYKCYIITSKGGKANLENYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPPQPTVVWASQVD
QGHNFSEVSNSTFELNSENVTKMVSVSLVYNTINNTYSYSCMIENDIAKATGDIKVTESEIKR
SHLQLLNSKASLQCVSSFAISWALLPLSPYIMLK

[illegible]

FIGURE 211

CTTCTGTAGGACAGTCAACGAGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCCTGCCAGGCTGTGCGAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCATCCTTGGGAGAAGTCAGCTCCAGCACCAATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
 AATCTAATGGAACCTTCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTCAGTAACGCCACCTGTCTAGTTCTGTCTGGTGAAGAACAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGCTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGGCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAAGGTCTGGGGCTGCACCTTGGCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCATTATTA
 AAGCACTGGTTCATTCAGTGCACCAAAAAAAAAAAAAAAAAAAAAAAAAA

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSLETVPVR
 LYQNMFCSAENCSEETHITAFTHVHVAEEHFHVFSQCCQGECSNTSDALDPPLKNVSSNAE
 CPACYESNGTSCRGPWKCYEEEQCVFLVAELKNDIESKSLVLKGCNSVSNATCQFLSGENK
 TLGGVI FRKFECANVNSLTPTSPATTSNHNVGSKASLYLLALASLLLRGLLP

FIGURE 213

GGCCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGAGGGAGCGAAGGTAGGAGCA
 GGGCTTGCCCTACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGCGGCGGGGCCAAGGCCGTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCCGAG
 CTACCGGAGCACCGCCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGCTGGCCGTACCCCTACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCAGTGCCAC
 TGCAAGTCGGGACCATGAGCCGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGACGGAGCACAAGCCTTGCACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCACTACCAGGACCACCACTACCCCTTCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGAAAA
 CACAA

MVPAAGALLWVLLNLNNGPRAAGAGQLTQTPTEMQVRVSLRFGGPMTRSYRSTARTGLPRKTRI
 ILEDENDAMADADRLAGPAAAEALLAATVSTGFRSSAINEEGDSSEGGVVINAGKDSTREL
 PSATPNTAGSSSTRFIANSQEPEIRLTSSLPSPRGRSTEDLPGSQATLSQWSTPGSTPSRWP
 SPSPTAMPSPEDLRLVLPWPWFHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQRLTEHKPC
 TYQQCPNCNRLREECPLDSTLCTDNCASQSTTSTRTTTTFFPTIHLRSSPSLFPASPFCALA
 FWKRVIGLEDIWNLSLVVFTEMQPIDRNR

FIGURE 215

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGGATGGCCGGCCTGGCGGCGCGGTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCCAGGGGACCGGTGAGCCGCGTGTACCGGAGCTGCGTACTGCACTGCGGAAGAGCA
 GAACCTGCTCTGGGGCGCTCTGAATCACTTCCGCTCCCGGACGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTGCGGACGACTGTAAGTATGAGTGTATGTGGGTCAACGTTGGGCTCTACCTCCAGGAAGGTACAAAGTGCCT
 CATGTCCATGGCAAGTGGCCCTTCTCCGGTTCCGTGTTCTTTCAAGAGCGGGCATCGGCCGTGGCCCTCGTTTCT
 CAATGGCCTGGCCACGCTGGTATGCTCTGCCGCTACCGGACCTTCTGGTCCAGCCCTCTCCCCATGTACCACA
 CTGTGTGGCCTTCGCTGGGTGCTCCCTCAATGCATGGTCTGTGTCACAGTCTTCCACACAGGGGACTGAC
 CTCACAGAGAAATGGACTACTTCTGTGCCTCCACTGTCTACTCTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CGTGGGCTGTCAGCACCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCTGTGCTGCTACTGTGACCGCTGCACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAAACGTGGCTATTGGCCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACACGCGGCGCTGCCTCAGCTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGTGTCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA
 TCTGGCACAATCAGCACCATCCCTGTCCACGTCCTCTTTTTCAGCTTCTTGGGAAGTACAGCGCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAGAGCCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC
 GCGCTGCTGGCCTCCCTTCTCCCTCAACCTTGTAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCTCCCAGCATCTGGGACTCGAGAGTGGGAGCCCTCTACCTCCTGGAGCTGAACTGGGTGGAAGTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCTGTTTCTCTCCACCAGCCTCTCTCCACATCTCCAGCTG
 CCTGGCTGGGTCTGAGGCCCTCTGTCTACTGCGGAGACAGGGACACAGGCTTAGGGATACAGGGGTCCC
 CTCTGTTACACCCCCCACCCTCTCCAGGACACCACTAGGTGGTGTGCTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACGGCGATTCTCCCATGGGATCTTGGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCACTCTGACC
 GTTGCCTTAGCCAGGTTCCAGGAGGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCAGCAAGCCAGGGCA
 AGGATCCTGTGCTGCTGTGTTGAGAGCCTGCCACCGTGTGTCGGGAGTGTGGCCAGGCTGAGTGCATAGG
 TGACAGGGCGGTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGCGCAGTGTGGAGACGGGTGTGT
 CGGGGAAGAGGTGTGGCTCAAAAGTGTGTGTGTCAGGGGGTGGGTGTGTGTAGCTGGGTTAGGGGACGTGTG
 TGCCTGTGCTGGTGGCATGTGAGATGAGTGACTGCCGCTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTCAACATCAATATCACTTGTGGAGCGCCAGCTCTGCCAAGAGCCGCTGGGCGGACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCCGTGTGTGCAATGTTCCCTGTCTGGTGCCCTTTGCCGCTCTCTGCAAC
 CTCACAGGTCCTCCACACACAGTGCCTTCCAGAAGCAGCCCTCGGAGGAGAGGAGAAATGGGATGGC
 TGGGGCTCTCTCCATCCTCTCTTTCTCCCTTGCCTTTCGATGGCTGGCCTTCCCTCCAAACCTTCCATTCCCT
 GCTGGCAGCCCTTGTCCATAGCTGATTTTGGGAGGAGGAGGGCGATTTCAGGGAGAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTCTTCTCCCTCCAGAGGCTCTACTCTCCAGGCTGGCCAGGCGAGGCGAGGGCC
 ACATATGCTGTGCTCTGGTAAAGGTGACCCCTGCCATTACACAGGCTTGGATGTTCTTCCCCACAGG
 AATAGAAATGAGGGAGCTCCAGAACTTTCATCCCAAGGCACTCCGCTGTGTAAGCAGGACTGATTTT
 CTCTGCCCTGACCCCTGTCCCTCTTTGAGGGAGGGAGCTATGCTAGGACTGCTTACCTCAGGCTCGGCT
 GCTCGCTAGCTTCTTTTGATACTGAAACCTTTTAAAGTGGGAGGGTGGCAAGGAGTGTCTTAATAATCAA
 TTCCAAGCTCAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMILLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
DAEVLVVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGGLQVVINGLNSTEPVKEYAAF
VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
GGQLQVRLTVQEKGEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
LELQDGEDEGYFQELIGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

TTCCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCCTCCTCCCGGGGTTCTGGGGTGACATTCAGCCGCGCCCTCTGTGGGTCGCGTTGCCACCCCA
CGCGGACTCCCCAGCTGGCGCGCCCTCCCATTTGGCTCTCTGGTACGGCCACACGCCCT
TTCCACCTTGACCAGCACTGGGGGCTGCGGTGTCTTTTCGGCTGCACTTTCGTGCGGTCGGC
CCCGGCTTCCGCGCTTTTCTGTACTCTGTGGTGGGGAGCCCGTTCGCGTTATCATCTCGTGT
CGAGGGGACATTTTCTGGCTGATCTCCTCTGCTCTGCGCTCTGTGCTGTGGTCACTCTCTGG
TCCATGTACAGCAGCGGCTCAGATGCGCGGCTCCAGTACGGCCTCCTGATTTTGTGTCTGCT
GTCTCTGCTCTTACAGGAGGTGTCCGCTTTGCCATCTACAAGCTGCTTAAAGAAGGCAGA
TGAAGGGTTAGCATTCGCTGAGTGAGGACGGAAGATACCCATCTCCATCCGCGAGATGGCCT
ATGTTTCTGCTCTCTCTCTCGGTATCATAGTGGTGCTCTCTCTGTATCAATATTTTGGCT
GATGACTTTGGGCGAGGTGTGGTGGGATCCATGGAGACTCACCTTATCATCTCTGACTTC
AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
CCTGTGAGAGGAGACGCTATGGGCTTTGGGCTGGTGGTGGGAGTACCTACATGACATCG
GGATGACATTTCTGAACCCCTGGTATGAGGCGAGCCTGCTGCCCATCTATGTCAGTCACTGT
TTCCATGGGGCTCTGGGCTTATCATACAGCTGGAGGGTCCCTCCGAAGTATTCAGCAGACC
TCTTGTGTAAAGGACTGACTACCTGGACTGATCGGCTGACAGATCCCCACTGCTTCTCCACTG
CCCATGACTGAGCCGACGCCGACCGCGGTTCATTGCCACATTTCTGTGCTCTCTCTGT
GGTCTACCCCACTACCTPCAGGGTTTGTCTTGTCTTTTGTGACCGTTAGTCTCTAAGGTT
TACAGGAGCAGCTGGGTTGACCGACTAGTGAATCTGTGGGTTTGAATCTGCATTTATCC
CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTCAGTGCTCTGCTCTAC
CGTGTAAAGACTACCTCCCTCCCTCTCGAGCGCAGCGAGGAGACAGTCCGGGTGAT
GGTGATTTCTGCCCTGCGCATCCACCGAGGACTGAGGAACTAGGGGGGACCCCTGGG
CTGGGCTGCCCTCTGATGTCTCGCCCTGATTTTCTCCATCTCCAGTTCTGAGAGTGCAG
GTTGCCAAGAAGGGACCTAGTTTAGCCATTTGCCCTGGAGATGAATTAATGAGGGCTCAA
GGATAGATTGAGCTCTGAGTTTCTCAGTATCCCTCAAGACTGGACATCTTGGTCTTTTCTC
AGGCTCTAGGGGGGACCAATTTTGGTGTGATAATAACCTAAATCGCTTTTCTTTTCTTT
GAGTGGGGGGAGGAGGAGGATATATGAACCTCTTAACCTCTTGGGCTATTTTCTC
TCTCGAGTTGCTCTCATGGCTGGGCTCATTTCCGCTCTTCTCTCTGGTCCCAGCCTT
GGGGGAAAGGAAGGAGTGCATGTTTGGCAAGCTGGCATCTAGGAACTAATGGTTTAAACCT
CCTTAACCAACAGCATCTCTCTCTCGCAAGGTGAAGTGAAGGAGTGTCTGGTGAAGCTGGC
CACTCCAGAGCTGCAGTGCCACTGGAGGATCAGACTACCATGACATCGTAGGGAAGGAGG
GACATTTTGTAGTTTAAATTTGGGTTGGGAGGGCGGGGAGGTTTCTATAAATGT
ATGATTTTCTGCTGAGGGTGGAGGTCTCCATCCTTTAATCAAGGTGATGTGATTTTGAAT
AATAAAAAAGAAATTTGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA

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FIGURE 220

MGA AV FFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGA AVSVLLQEVFRFAYYKLLKKADEGLASLSE DGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSPIYYFLTSAFLTA AII LLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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100
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FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

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FIGURE 223

NGTTGGAGAAGTGGCGCGGACNNTTCATTTGGGGTTTCGGTTTCCCCCCTTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGCCCGGCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTCATCTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCTCTCCATCCGCCAGATGGCTATGTTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTTCCCNITCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTCCTGTCTGGTCAGGCCCCCACCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCAGGGAGCAGTGGGTGGTTATACTCAGGCCCGGTGCCCAGAGCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTTGGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GGCTACAGCAAGACCCC
 CCTGGATGTGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTCCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGTCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACGAACAGAGAAGTTCGTCCCACTAAAGATGTGAGCCCAT
 CAACGCTCTCCTCTCATTTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGACAA
 CCAAGAGCCCCAAGTGCACCTCCCTAAGGTCCCTCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGGACTCGTGTCTTGGGGAGATTACCCCTTGTCGCCGGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGATCCAGGAAACCATCCAGGCCAAGTCT**TGA**GTGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGCTCTCTAGTTGAACCTGG
 GAACAATTTCCAAACTGTCCAGGGCGGGGTTCGCTCTCAATCTCCTGGGGCACTTTCAT
 CCTCAAGCTCAGGGGCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQFWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRIIPTKDVRPINVSSHCPISAGTKCL
VSGWGTTKSPQVHFPPKVLQCLNISVLSQKRCEAYPRQIDDTMFCAGDKAGRDSCQGDSSGGP
VVCNGSLQGLVSWGDPNRPNGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGTGCCAACTTGAGGACCGGCGCGCGCA
 CAAGCCGCGAGCGGCGAGCTGCGGCTACGTGCTGTGCACCGTGTCTGGCCCTGGCTGTGC
 TGTGGTGGTGTAGCTGTCAACCGGTGCCGTGCTTCTCTGAACACGCGCCACGCGCGGGGCACG
 CGCGCCCCACCTGTGCTGACGACTGGGGCTGCCAGCGCCCAACAGCGCCCTGGTCACTTGGA
 AAGGGCGGACAGCTCGCACTCTCAGCATCTCTATTACCCGCGCTGCCCGGACTCACCAGACA
 GCTTCGCACGCTGGAGAGCGCCAGGCGCTCGGTGCTGCAGGCGCTGACAGAGCACAGGCGC
 CAGCCACGGCTGGTGGGCGACAGGAGCAGGAGCTGCTGGACACGTTGGCCGACCGACTGCCC
 CCGGCTGCTGGCGCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCGATG
 GCACGCTGGGCGAGGCGCTCAGCGCCCTGCAGAGTGAGCAGGGCGGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTCAGCGACATCTGGATGCCCT
 GCAGAGGGACCGGGGCTGGGCGGCGCCCGCAACAGGCGGACCTTCAGAGAGCGCCTGCCCG
 GGGGAACCGGCGCGGGGCTGTGCCACTGGCTCCCGGCGCGGAGACTGTCTGGACGTCTCTC
 CTAAGCGGACAGCAGGACGATGGCGTCACTCTGTCTTTCCACCCACTACCCGGCGGGCTT
 CCAGGTGTACTGTGACATGCGCAGCGGCGGCGGCTGGACGGTGTTCAGCGCGGGGAGG
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCACC
 GGGGAGCAGTGGCTAGGGCTCAAGAGGATCCACGCGCTGACCAACAGGCTGCCACAGCT
 GCACGTGAGCTGGAGGACTTTGAGAATGGCAGCGCTATGCCCGCTACGGGAGCTTCGGCG
 TGGGCTTGTCTCCGTGGACCTTGAGGAAGACGGGTACCGCTCACCCTGGCTGACTATTCC
 GGCACCTGCAGGCGACTCCTCTCTGAAGCACAGCGGCATGAGGTTACCAACCAAGGACCGTGA
 CAGCGACCATTCAGAGAACAACCTGTGCCGCTTCTACCGCGGTGCCCTGGTGGTACCGCACT
 GCCACAGCTGCAACCTCAATGGGCGAGTACCTGCCGCGTGCACAGCTCCTATGCCCGAGCG
 GTGAGTGGTCTCTCTGGACCGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCGGTCGGGAGGACCG**TAG**ACTGGTGACCTTGTCTTGGCCCTGCTGTGCTCTTCGCG
 CCACTCCCGACCCCACTCTCACTCTTTCGTGAATGTTCTCCACCCACTGTGCCCTGGGGAG
 CCACTCTCAGTAGGGAGGGCGGGGCCATCCTGACACGAAGACTCCTGGCGCGGGGAGT
 CACACATCGCCTTCTCGCGTCCCGACCCCTCCATTTGGCAGCTCACTGATCTTGTCCTC
 TGCTGATGGGGCTGGCAAACCTTGACGACCCCACTCCTGCTGCCCGCTGTGACTGCCG
 TGCTGTTTGGCGTCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGACCCCTTCCCTTCCCG
 GGCCAAATACCGGCAATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCTGGAGTCCCT
 CTAGCAGATCGTGGGAATGTGAGGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCTCCAG
 CCTCCCAATGCCAACCACCCCGTTTCCCTGGTGCCAGAGAACCACCTCTCCCCAA
 GGGCCTCAGCTGGCTGTGGGCTGGGTGGGCGCATCTTACCAGGCCCTGAGGTGAGGATGGG
 GAGCTGCTGCCCTTTGGGACCCACGCTCCAAGGCTGAGACAGTTCCCTGGAGGCCACCCAC
 CCTGTGCCCGGCGAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCCACTGCTCTCTG
 TCTCAAATGAGCGCCCAACCCATCCCGACCCAGCTCCCGGCGTCTCTTACCTGGGGGAGC
 CGGGGCTGCCATCCCATTTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGAATCGCTAATGGGAAGCTCTTGTTTTCTGGGCTGGGGCTAGGCAGGGCTGGGATGAG
 GCTTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCCTTGGC
 ATTGACGCTGGCCACTGGACCCAGGCGAGGCGCGCGCGGCGAGTGGTCAAGGGACAGGGA
 CCACTCAGCGGCAAAATGGGGTGGGGGACTGGGGCAGCAGACAGGCAACCTGGACA
 CTTTCTGTTGAATCTCCCAACCCAGCAGCGTGTATCCCCACTCTTGTGTGCACACA
 TGCAAGGTGAGACCCGAGGCTCCAGGACAGCAGCAGCAAGAGGCGAGGCTGGAGCGGG
 TCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCCTTACCTCAGGCCAGATGAGGG
 CGGCTTTTCAAGGCTCTGATGGGGGCTCCGAAGGGCTGGAGTCAGCTCAGCCTTGGGAGCT
 GCTTACGAGCTCTCTCGGGAGGAGGGGAGGTTCTCTCCAAAGGACACCCGATGGGA
 GTGCGCTAGGGGCTGCGGGTTCCTTCTCCCTCCCTCAAGTTTGTGCTTAAAA
 AACAAATAAATTTGACTTGGCACCAGCTGGGGGTGGTGGGAGAGGCGGTGTGACCTGGCTCTC
 TGTCCTGAGTCCACAGGTCATCCACATGGCGAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLRLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSSLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTGTAGTCCT
 TGCTTCCTGAACTAGCTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACAGGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAAGCTGGCGACCAGTGGCCCTGACCTGTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGCTGCTGAGCTGTATAACAAAGCTGGAGCACACAGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAGACAGCAAAAGTTGGGAG
 GACTGTAATAATTTCTGCGCTTAGTGAAACTCTACCATGCTGAAGATAAAACAAACAAGAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTACCAGCCCAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTATGCACGTATTAAACAGTCACA
 AGAAGTCTTATTACATGCCACCAACCAACCTCAGAAACCCATAATGTATCTGCCTTCTTG
 GCTTAGAGATAACTTTTGTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCCTTACACTTGGTGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTGTACC
 AGCAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTGTGCCATTAAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAATGTAAATACTGTGAAAA

FIGURE 230

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSRPRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGED



FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

FIGURE 232

GCCGAGCGCAAGAACCTCGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCCCGCCGCGGGG
 CCCGAGCCTCCGGATCCGCCCTTCCCGGTTCCCGCCCTCGGAGACTCTCTGGCTGCT
 CTGGGGGTTTCGCCGGGGCCGGGACCCGCGTCCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGCCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCACTGAGCCT
 GCTCAGCGTCACTGGGTGAGGAGCCGTGCGGCCAGGCCGCCCACTCGAGACTCTG
 AGCTGCCCGCGCGGCAACACCAACGCGGCGCGCGGCCCACTCGGTGACGCCGCGAGCG
 GAGCGCGAAGAGCCCGGGGCGGCGAAGGCGCGCGGGGAGAATTGGAGCCGCGCGCTCTTGCC
 CTACCACTGTCAGAGCCCGGCCAGGCCGCCAAAAGGCCGTGAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGCCGCTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCAGCTGGGCGACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCAGGGGCGCGCGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGCGGACGACTTTGAC
 TGGTTCTTCTCGTGGTGCCTGACACCACTTACACCGAGGCGCAGCGGCTGGCACGCTAACTGG
 CCACCTCAGCCTGGCCCTCCGCGGCCACCTGTACTGGGCGGCCCCAGGACTTTCATCGGCG
 GAGAGCCCCACCCCGGCGCTACTGCCACGGAGGCTTGGGGTGTGCTGTGCGCATCTGTG
 CTGCAACAAGTCGCGCCCACTGGAAGGCTGCCGCAACGACATCGTCAGTGGCGGCTGGA
 CGAGTGGCTGGGTGCGTGCATTTCTGCATGCCACCGGGGTGGGCTGCACTGGTGACCAAGG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGAGCCAGTGCAGAGGGGACCCTCAT
 TTCCGAAGTGCCCTGACAGCCACCCCTGTGCGTGACCTGTGCACATGTACCAGCTGCACAA
 AGCTTTTCGCCCCGAGCTGAAGTGAACGCGACGTACACAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACAGCCATCTGGCCGTTGATGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT
 CCAGCACCATTCCCGCCCGGCTCCCGCTTTGAGGCTGCTGCGCTGGGACTACTTACCGGAGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCGCTGCCCATGCTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACCAACCGGCGCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGA
 ATACAGCTGAGACTTGCAGCTGGAGGCACTGACCCCCAGGAGGCGCGCGGCCCTCACTC
 GCCGAGTGCACTGCTCCGCGCGCTGAGCGCGGTGGAGATCTTGCCCTTGCCCTATGTCACT
 GAGGCTCACGTCTCACTGTGCTGCTGCTCTAGCTGCGGCTGAGCGTGACCTGGCCCTGG
 CTTCCTGGAGGCGTTTGCCACTGCGAGCACTGGAGCTGGTGATGCTGCGGCGAGCCCTGACC
 TGCTGCTACTGTATGAGCGCGCCAGGCCAGCGGCTGGCCATGCAGATGCTCTTCGCACCT
 GTCAAGGCCACGTTGCGCAGAGCTGGAGCGGCGTTTCCCGGTTGCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCCGACCCCTCACCCTGCGGCTCATGGATCTACTCTTCAAGAAGCACCCGCG
 TGGACACACTGTTCCTGCTGCCCGGGCCAGACAGCTGCTCACGCGTGACTTCTTGAACAGGAGAGG
 TGCGCATGTGATGGCATCTCCGCTGGCAGGCTTCTTCCCATGCATTCCCAAGCCTTCCA
 CCCAGGTGTGGGCCACCAAGAAGGCGCTGGGCCCCAGAGCTGGGCGTGACACTGGCGGCT
 TTGATCGCCAGGACGCGGAGGCGCTGCTTACAACCTCCGACTAGCTGGCAGCGCTGGG
 CGCTGGCGGCGAGCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCTTGGATGTGTACGAGCT
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCGGCGCTGCTGCAGCGCT
 ACCGGGCCAGACGTGCAGCGGAGGCTCAGTGAGGACCTGTACACCGCTGCTCCAGAGG
 GTGCTTGAAGGCGCTCCGCTCCGGAACCCAGTGCCCATGCTACTTCTTGAACAGGAGAGGG
 CAACAGCACCT**G**ACCCCACTGTCCCGTGGGCGTGGCATGGCCACACCCCACTTCT
 CTCGCCAAAACAGAGCCACTGCCAGCCTCGCTGGGAGGCTGGCCGTAGCCAGACCC
 AAGCTGCAAACTGCTGCTCTGCTGCTGCTGGGCTCCCTGGGCTTGGACAAGCATCTGGG
 GGAGCTGCCCGCAGAGCCACCACTTCTCATCCAAACCCAGTTTCCTGCCCTGAGCCT
 GCTGATTGGGCTGTGGCCTCCAGTATTTTACGATACAGTCTGCTGACGCGAGCCCTGC
 CTCGGGCGCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAGGAGGAGCTGAGGAGGG
 GCATCTCCCACTTCTCCCTTTTGGACCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGF TSLLSVTWVEEPCGPGPPQPGDSELP PRGNTNAARRP
 NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKAVRTRYISTELGIRQLLVAVL
 TSQTTLPTLGVAVNRTLGHRLERVVFLTGARRRAPPGMAVVTLGEERPIGHLHLALRHLL
 QHGDDFDWFFLVPDTTYTEAHGLARLTGHL SLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
 VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGR CILDATGVGCTGDHEGVHYSHLELSPGEP
 VQEGDPHFERSALT AHPVRDPVHMYQLHKAFARAE LERTYQEIQELQWEIQNTSHLAVDGDRA
 AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTAL EELN
 RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
 LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
 HADVFA PVKAHVAE LERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
 TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQPGGPPPELGRDTGRFDRQAASEACFYNS
 DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
 YHRC LQSVLEGLGSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAAATTCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTGGAAGCAAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCCCTGAGACCCTGCAGCACCATCTGT**CATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGTCTTTTGGCGCGAGGCGACGCGAGGGCTCCCGGCCCGCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCAGGAGACGAAAACCTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGTCTCTT
 CTTTGGCGTCTCCATCATCTGGTCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTCCCATCATGGAATCAAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACC GCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGCTTCGACCCAGCA
AGATCCAG

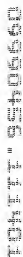


FIGURE 237

GCGGCGGCTATGCGCGCTGTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTGCATACCCCGCTGCCTTCCGGGG
 ACGTAGCGCCACATTCCAGTTCGCGACGCGCTGGGATTCGGAGCTTCAGCGGGAGGAGTG
 TCCATTACAGGCTCTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCTTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCTGTC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACACAGCTACCACTCCCAAGGCAGTGATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCGTGTCAAGTTGATTTGATGCCTTC
 ATCAGCGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTCAGCGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATACCACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTATCCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGAAGAGACCCCAAGAGAATGAGGCCCCCGCAGTGCCTTCTGTC
 ATGCCACGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGAGCTGAGCACACTGCTGTAC
 AACCCACCCATACCGGGCCTTCCCGGTGCTGCTGGACACCGTACCCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGTGCAACCCACCTCCTGGAGATGCTGATTACAGCTGCCG
 GCCAACTCAGTCAACAAGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCTAACCATGGCTTCTATGTACGCCATCTGCTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAGCCAGTGGACTGGGAAGAGAGTCCCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCGCTCAGCTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCAGGAGAGCCCGCACAGGT
 GGCTTGGCCAAGCGCTGGCCAACTTATCCGGCGCGCCGAGGTGTCCCCCACTCTGATT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCTCAGAGTTGGCTTTTGAACCAAGTGCCTGGACAGGTCAAGGCG
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGACCAATGTGGCATTTGAATTTGAATTA
 CTTAGAAATTCATTCTCACCTGTAGTGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGATTGGACAGCAGCAAAAAAGATTTCCATCACCACAGAAAAGT
 GGTGCGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRNARCTSSISWELRQTLVSVFDFITG
QGKKDWSLFRMFSLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLDDTVPWYLRLYVHTLTITSGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSMFYNVICLTCTVVAVCYGSFYNNLTTRTFHIEEPTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCAGCAGCTTCTTGCTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTCACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCTTGATCTTGGACTTCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEggnKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

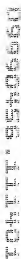


FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTTGTTAAGACAAGGGTGTGCACCTTCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCTGCCTGTGGAGATGCAGGCACCTGAGGCCAAGG
 CGTCCAGTGGTCTTGTCTTCTGGCTGTCTGGTCTTCTTCTCTTCGCCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAAACCTCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAGGAGGCCAACAGGCACCCGCGAGGAGCAGGACAAAGGTGCCCCAC
 ACAGCCAGAGGGCAGCATGGAAGAGCCAGAAAAAGAAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGCCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACCCAGGGCAAGCGGCAACCCAGCCAAAGACGCTCATTTCCCAAAAGTCA
 GCACAGAATGCTGGCTCCCACAGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCCAACCCCTGCCCTTTCCAG
 AGCCCCAGCAGCAGAGAAACCAAGACTGAAGGCCGCCAATTCAAATCTGAGCCTCGGTG
 GGAATTTTGAAGAAAAATACAGCTTCGAATAGGAGGCCCTTCAAGCAGCTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCTGCTGTGGCTCCAGAAACTCTTTCTGCCAACCTCACTCTC
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAAGTCTGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGACATCACTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCTCTTGGGAAGGACGCTCCGCTACTTGCACCTTCTTGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAAGGCACAGACCCAGGAAGCTTTTGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAATCCGGCTGTACACGCGTCCCTGGTC
 CCGGAACCTGCCAAAGCCAAAGAACT**GA**CGGGGCCAGGGCTGCCATGGTCTCCTTGCCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTCTTGAAGTTCTTCACTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTTTAATTAAATGGGGTGATGGGTGGCCAAATACCACAAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGTCTAGAAGACTTTTCTAGGAGTTATCTGATTTAGAGGGTCTATCTACTTGTCTTG
 TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAACCTGATAATAACAAATGATTGTT
 GTCCATGAAAGGCCAAATAAATTTTCTACAGTGAAAAAAGAAAAA

FIGURE 242

MRSCLWRCRHL SQGVQWSLL LAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLS PRGQDAGMASGRTEAQSWKSQDTKTTQNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPKEKKPQATPPPAPFPSPPTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLF LPNLTLFLDSRHF
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGF TAFSLTQSL LILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLHPDFL
 RYMKNRFLRSKTL DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKR LHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CGATGCGCGGACCCGGGCACCCCTCTCTCTGGGGCTGCTGCTGGTCTGGGGCCTTCGCCG
GAGCAGCAGAGTGGAATTTGTTCTCTGAGATCTGAGGATGAAGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGACAACTTCCATAGACTTTATCACACA
CCAGAGACTGCACCATTCTCGATACTATAAAAGATGCGCCAGGCTTCTTTACCCGGCTGGCT
GTCAGTCCAGTGTGATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCG
ATGAGAAGTGCCCTGGAAACCAACAGGGAACAGCAACTCTTTATACACATCCCTCATGG
ACAAGAGATTTTATTTTGACAGAGACTCTCCATAAGTCTCTTTGATTTTGTATGTTGTG
ACAGTTTCAGATATATATTCGATAAATCAGTGACTTGACAGTGTTATCTGTCACTTATT

Figure 10. The effect of the initial concentration of the monomer on the polymerization of α -methylstyrene initiated by TiCl_4 in CH_2Cl_2 at -78°C . The concentration of the initiator was 1.0×10^{-2} mole/liter. The polymerization was carried out for 10 min. The polymerization was terminated by the addition of methanol.

Figure 10. The effect of the initial concentration of the monomer on the polymerization of α -methylstyrene initiated by TiCl_4 in CH_2Cl_2 at -78°C . The concentration of the initiator was 1.0×10^{-2} mole/liter. The polymerization was carried out for 10 min. The polymerization was terminated by the addition of methanol.

Figure 10. The effect of the initial concentration of the monomer on the polymerization of α -methylstyrene initiated by TiCl_4 in CH_2Cl_2 at -78°C . The concentration of the initiator was 1.0×10^{-2} mole/liter. The polymerization was carried out for 10 min. The polymerization was terminated by the addition of methanol.

FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCCGCGCCAGCCCCACCAATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTCTGGGGGCTCCCTTGGTGTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTACCTTCT
 GCTGCGGGACCTGTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTGCTGTGGTTGCCACCACCATCTGCTGCTTCTCTGTTCTGTTGTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCTGCACTCCTCCTCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCTCGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAAC TAGA
 ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTCACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTGACGAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYNPAAPPP
YMPQPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

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CGGGGAGGCTAGGCCCGCGGAGCTGGTGGTGGCGGCGGCGCAAGGGGTGAGGGGGGCCCCAGAA
CCCCAGCTAGTAGAGCAAGAAGATGGCTGTTTTCGCCCTCAAAATGGTCCCTTGCAACCACTG
TCATTTCTACTTTCTCCACGTCTGGTCTCTTCTACTCTGTGCATCCTCTCATGGTGTGACAG
CACTGAAGCACTCTCCAAAGCTAGTATGACGGACACCAATTCCTTTGGAAATAAAATACGACTTC
CTAGTAGCTGTCATCCCGAGTTCATTATGATCTCTTTGATCCATCGAACCACTTCCACCGCTGACC
TTCTTGGGGGAACCCAGAAAGTAGAAATCACAGCCAGTCAAGCCACCCAGGACCATCATCTCGCA
TAGTCAACACCTTCGAGATATCTAGGGCCACCCCTCAGGAAGGGGAGCTGGAGAGAGGCTCATGG
AAGAACAGCTCGAGGCTCGGAACACCCCTCTCAGGAGCAAAATGTCATGCTGGCTCCCGAG
TTCCCTCTTTGTGGGGCTCCCGTACACAGTTGTCTATCTACGTGGCAATCTTTCCGGAAG
TTTCCCGGATTTTACAAAGAACCTCAGACAAAGCAAGGAAGGGGAAGCTGAGGATATACGACA
CAACACAAATTTGAACCCACTCGAGCTAGAAATGGCTTTCCCTTGATTTGATGAACCTGCGCTT
CTGACCAAGTTCTGACCAATTTTGAAGAGAGCGCAAGGCACTAGGACATCTCCAAATATGG
ATTGGTGAAATCTGACGCTGCTTCTGAAGAGGACATCAGGAAGACCAATTTTATGTCACTGTGA
AGTGGCGCATCTGAGCTGCTCCCAACACCTCAGATTTTGGTCTCTCAGCAGAGATTAAC
AGGATGGAGTGAAGTGTTCCTTTATGTGTGTGGCAGACAGAGATAAATCAGACAGATATGC
ACGGAGTGTGGGGTACTCTCTAGTCTTTTTCAGATATTTCTAGCATATCGGATCTCGCC
TACCAACAAAGATCTTGTCTGCTATCTGGCTTCTTACGTCTGGTGCTATGGAAATCTGGGA
CTGACACCAATAGAGAACTGCGCTGTGTGTGATGACAGAAAGTCTTGTCATCAAGTAA
GCTTTCGCACTCAGTGTGTCGCCCATGAACTGGCCCAACAGTGGTTTGGGAAGCTGTGTCAT
CTATGCAATGGTGGTCTCTTTTCTTAAATGAGGATATGCAAAATTTATGGATTTGTG
TCTGTCAGTCTGGACATCTTGAACTGAGGATGAGATTTTGGCAAAATGTCGAA
CGCAATGGAAGGAGATCTTAAATTCCTCAAGTCTGTCATGATGATGATGATGCTGCG
CTCAGGTGAGTATCTTGATGATGTTTCTTATGATGAAGGAGCTTGATTTCTGAATTA
CTAAGGAGGATCTTAGCGCTGACGACTTAAAGATGGTATGTCACAGTATCTCAGATACG
TAGCTATAAAATAACAAAGAACGAGGACCTGTGGATAGTATGGCAAGTATTTGCCCTACAG
ATGCTGTAAAGGGATGAGTGCTTTTGCCTAGAAGTCAACATCTATCTCATCTCATACT
TGGCATCAGGAAGGGGTGGATGTGAAACCAATGATGAACACTTTGGACATCAGAGGGGTTT
TCCCTTAATAACCATACAGTGAAGGGGAGGAATGTACACATGAAGCAAGACCATCATGTA
AGGGCTCTGACGGCGGCCCGGACACTGGGTACCTGTGSCATCTTCATATCATCTATCC
AGCAAAATCAACATATGGTCCATCGATTTTGTCTAATAAACAAACAGATGTGCTCTCC
AAGAGAGGTGGAAATGGATCAAAATTTAATGTGGGCATGAATGGCTATTCATTTGTGCATAGC
AGGATGATGGAATGGGACTTTTGACTGGCTTTTAAAGGAACACACACAGCATGACAGCT
AATGATCGGGCAAGTCTTATTAACAATGCATTTCAAGCTCGTCAGCATTTGGGAAGTGTGCAT
TGAAAGGGCTTTGGATTTATCTCTGTACTTTGAAACATGAACATGAATATTGCCCGTGTTC
AAGGTTTGAATGACGTATCTCTATGATTAAGTTTAAATGGGAAAGAGATATGAATGAAGT
GAAATCTCAATCAAGGCTTCTCTCATCAGGCTGCTAAGGACCTCATTTAGATGACAGCATG
TGACAGACAGGGCTCAGCTCTCAGAGCAAAATGCTGGGAGTGAACTACTCTCTCGCTGTG
TGCAACAACTATCAGCGTGGCTACAGAGGGCAGGAAGGCTATTTCAAGAACTGGAAGAAATCC
AATGGAAATCTGAGCTCGCTGTGCAAGTGAACTTGGCAGTGTGTTGCTGTGGGGGCCAGAG
CACAGAAGGCTGGGATTTCTTTATAGTAATATCAGTTTCTTTCTCAGATATGAGAAAA
GCAAAATTTGAATTTGCCCTCTGCAAGAACCAAAATGAAGAAAGCTTCAATGGCTATAGAT
GAAAGCTTTTAAAGGAGATAAAATAAAACCTCAGGAGTTTCCACAAATCTTCACTAATTTGG
CAGGAACCCGATAGGATACCACTGGCCCTGGCAATTTCTGAGGAAAAACTGGAACAAATCTG
TACAAAAAGTTTGAACTTGGCTCATCTTCATAGCCGACATGTAATGGGTACACAAATCAA
TTCTCCCAAGAAAGACGGCTTTGAAGAGGTAAAAAGATTTCTCAGCTCTTTGAAAGAAAATGG
TTCTCAGCTCGGTGTGTGCTCAACAGACAAATTTGAACCAATGAAGAAAAACTCGGTTGGATGG
ATAAGAAATTTTGATAAAATCAGAGTGTGCTGCAAAAGTGAAGAGCTTTGAACGTATGTA
TTCTCCCTCTGGCCGGTCTCTGTATCTCTAATCAACCAAAATTTTGTGTAGTGTATTTTCAA
ACTAGAGTGGCTGTTTGTGCTCAACTGGAGATACTTTTCCTTCAACTCATTTTTTGA
CTATCCCTGTGGAAGAAATAGCTGTATGTTTTCATGAATGGGCTTTTTCATGAATGGGCTA
TCGCTACCAATGTGTTTGTTCATCAGCAAGTGTTCGCCCTGCAACGTAAACCAAGTGTGGGT
TCCCTGCCACAGAGAATTAAGATACCTTATTTCTTCAAAAAAATAAAAAAATAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFTGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEPLQVLE
 HPPQEIQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASFSSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMFVSVSVTHPELVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKEKRDMEVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNEKELQWLLDESFKGDKIKTQEFQILTIGRNPVGYPYPLAWQFLRKNWNKLVQKFELGS
 SSIAHMMVGGTTNQFSTRTRLEEVKGFFSSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCCAGACGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGGTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATCCACTCAGCCCCCTCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTC
 CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GGCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTGTGTTGAACACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCAGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGAGACACAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCACACACAATCATTATCTACTACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLRGGGIFSNLRVQGCMPPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCNSASSSSVLLN
SLPPQAAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCCTGCCTGCCTG
 CAGCATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCCTTCCTGTCCTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCTG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTGCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATGTGAGCCTCAGGCTGGGGCTGCCCATTTGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGTTGGAG
 GCTCACTGAGTAGAGGCTGTTGTCTAAACTGAGAAAAATGGCCTATGCTTAAGAGGAAAAATG
 AAAGTGTTCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

MRGNLALVGLISLAPLSLLPSGHQPAGDDACSVQILVPLGLKGDAKEGDKGAPGRPRGRVG
PTGEKGMGMGDKGQKGSVGRHGKIGPTGSKGEKDSGDTGPPGPNGEPLPCECSQLRKATGE
MDNQVSQLTSELKFIKNVAVAGRETESKIYLLVKEEKRYADAQLSCQGRGTLSPMKDEAAN
GLMAAYLAQAGLARVLFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYYDEEDCVEMVAS
GGMNDVACHTMYLMFVFEDKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCTTGATCCTGCCAGACCACC
 CAGCCCCGGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCTTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCAGAGAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTTCGGCCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCTGGGAACAGAGGAGCAGAGACC
 TTTATAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT
 ATCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACATGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTAGAGTTCCTGTAGTGT
 CCTACATTAATAATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDHDFVGLMGKRSVQPEGKTPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCGCTGTGCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCTGCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCGAGGAGTGGAGCC**ATGA**GCTGCGTCTCTGGGTGGTGTTCATCCCCCTTGGGGC
 TGCTGTTCTGCTGCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCSTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCATGCCCCTG
AAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAATCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGACAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGAGGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCAACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGAGAGTCTTCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAACCTTCCTTCCTGGCTGGTTTTCCAGAATAACAGAGGAATGGACCACAGTCTTCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTACGTATGAATGGCTT
 TTTAAACAAACCCACGTCCAGCCTGGGTAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTG
TGTCTTCTTGGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAAGTGTGAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCC
CTCCGATTGTTCTAAATAAATTGAAAGATGTCTGCTGTGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTACGCTA
GTAAATAGAAACCTGTGTTTATTCAGGTATTTTAGAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAACACAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGAGG**GATG**ATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCTTGCAGCTTTTCGCCCCGCCGAGTGAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCAAGCAACGAGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCTAGTCTGGGAAGATGTAGACCTACACAAGTGAGTACAAGAGTGCACTGGGTAACTT
 GGCAGTGAAGCTGACCGTCCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGAGCTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCAAAGGTGTACTTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAACTCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTCTATTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATAAACCCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTTCATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCCCTGCATCTATGATCCACTGGGCACATACAGTAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCCTGGAATGAAGGAACAGATCATTACAAACTCCAGACAAGAGAAA
 GCTGCCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTT
 TACAGGACAGTGAGGCTATAGCCCTTACAAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCCTCTTTCCCAATGTCACTGCGCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTTTTACT
 GCTCCCCAGCATTACTGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCCTAATATTACCAGCTGGCTTTTCTCTCCCTGGCCCTTGTGAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCACTAAAAATACATTAAATATTCTTT
 CTTTTCTTTTCTTTTTTTTGGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACTCC
 AGAGCTCAAGAGATCCTCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACTATTCTTATTGAGGTTTAACTCTATTTCCTCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAGTGAAATATTAACATTGAATATCGCTTT
 CCAGTGTGGGAGTGTGTCAGATCATTTGAATTTCTCGTTTACCTTTGTGAAACATGCACAAG
 TCTTTAGCTCTGATCTCAGATTTAGGTGAGTAACACAATTCAAGGTGAAAGATACAGC
 TAGAAAACTACTCAAAATCCCATAGTTTTCCTATTGCCCAAGGAAGCATCAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTTTACGCTCAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTTCATGCTGTCACAAGACCTTCAATAGGCCCTTCAATGATTAATTCCTCC
 AGAAACCAAGCTTAAGGGTGAGGCCCACTCTAGCCTCCTCTGTCTGTCTGCTGCTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKIRTLNASC DNMLGKSLKIVKKMMDTHGSMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPA PRKQILTL SWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEP GTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGP HRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIWLVLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTHAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTACCCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGTCTGACTGTGCTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCGAGCACCTGTCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGTCTGCCAACCTGCTGTGCTCCAGGTTCGCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTCTTCCCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTTGGCCTGACCCTCAGGCCCTTACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTATCTTCCCTCGATTGGTTAACTCCTTAGTTTACAGCCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTACCAGT
 TAACCAGTGAAGCCCCAATTCCACAGCTTTTCCATTAAATGCAAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

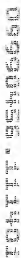


FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGCGCGCAGAAAGGGAGGCACTTGAGAAATGTCTTTC
 CTCAGGACCCAAAGTTTCTTCCCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCCTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCGTGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCAGAGAAAAAGAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCCTCAGAGAAAAATGA
 TGTGTGAAACTGCCAGCTCAGGGATAACCGAGGACATTACCTGTGTTTCATGGGATGTATT
 GTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCTAAGGCAAAATAGCCCCAAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTTGAGGTGCGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 269

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC
GGCCAGGTGCCCCGTGCGAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCCTGCCAACCCGCCACCCAGCCC**ATG**GGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAAGGGCTGCCTGCCCAT**CTAG**GTCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTC AATAACATTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTCTGTCTACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAAATGTTGCCAAGGAAAAAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTTATTAGAGGTTTGTCTTCTTAGTTCT
 GTGGCTGCTGCACCACTCAAACTCTTCTTATTAAGCTGAATAATAATGGCTTTGAAAGATA
 TTGTCAATTGTTTAGATCTTAGTGTGCCAGAAAGTAAAAAATTAATGGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACTCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTAACTTCTGAGAATTGGAGAGAAAGGCGAATACATTCACTTCACTCCCTGACCT
 AAAACCAATAAATCTGCTGATGTTATAGTTGCCACCACCTACACTCCCGAGGTAGAGATGAACCA
 TACACCAAGCAGTTACAGCAATGTGGAGAGAAAGGCGAATACATTCACTTCACTCCCTGACCT
 TCTACTTGGAAAAAACAAATGAATATGGACCACAGGCGAACTGTTTGTCCATGAGTGGG
 CTCACTCCGGTGGGGAGTGTTTATGAGTACAATGAAGATCAGCGCTTCTACCGTGTAAAG
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGCGAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCGAGCTGCTTAGTAGAGCATGCAGAAATTGATTCTACAAACAAAACGTATG
 GAAAAGATTGTCAATTCTTTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCTGTTGTTGAATTTGTACGAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTCTGAGGATT
 TTAAAAACACCATACCCATGGTGACACCCTCTCCACCTGTCTTCTCATTTGGTGAAGATC
 AGTCAAAAGAAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAAGGACCGCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGG
 TGGGATGTTTCACTTTGATAGTACTGCCACTATTGTAATAAGCTAATCCAAATAAAAAGC
 AGTGAGTAAGAAACACACTCATGGCAGGATTACCTACATATCTCTGGGAGGAATCCAT
 CTGCTCTGGAATTAATATGCAATTCAGGTGATTGGAGAGCTACATTTCCCACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAACTGCAAGTCTCTGTATTGATGAAGTG
 AAAACAAAGTGGGGCCATTGTTTATTTATGCTTTGGGAAGAGTCTGCTGATGAAGCGATTAAT
 AGAGATGAGCAAGATAACAGGAGGAAGTCAATTTTATGTTTCAGATGAAGCTCAGAACCAATG
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAAGTCCCTT
 CAGCTCGAAAGTAAGGGATTAACTGAAATAGTAATGCCGTGGATGAAGCAGACTGTCAATAT
 TGATAGTACAGTGGGAAGGACACGTTCTTTCTCATCAGTGAAGCAGTCTGCCTCCAGTA
 TTTCTCTCTGGGATCCAGTGGAAACAAATAATGGAATAATTCACAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCAGGAACTGCAAAAGGTGGGCACTTGGGCAATCAATCTTCAAGC
 CAAAGCGAACCCAGAAAACTTAACATATTACAGTAACCTCTCGAGCAGCAAAATCTTCTGTGC
 CTCCAATACAGTGAATGCTAAAATGAATAAGGACGTAACAGTTTCCCGAGCCCAATGATT
 GTTTACGCAAGAAATTCACAGGATATGTACCTGTTCTTGGAGCAATGTGACTGCTTTTAT
 TGAATCAGAGAAATGGACATACAGAAAGTTTGGAACTTTTGGATAATGGTGAGGCGCTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAGTTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATACGGGCTCCACT
 GAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATGGAAGCAAAACCCGCGAA
 GACCTGAAATTTGATGAGGATACCTCAGACCCTTGGAGGATTTGAGCGAAGCAGCATCCGGA
 GGTCAATTTGTGGTATCACAACTCCCAAGCCTTCCCTTGCTGACCAATACCCCAAGTCA
 AATCACAGACCTTTGATGCCACAGTTTCATGAGGATAAGATTATTTCTACATGGACGACACCG
 GAGATCAATTTTATGTTTGGAAAAGTTCAACGTTTATCATAGAATAAGTGCAAGTATTTCTT
 GATCTTAAGAGCAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTACACCAAGGA
 GGCCAACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCC
 ACATATTTTATGCCATTTAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACT
 GCACAAGTAACCTTTGTTTATCCCTCAAGCAAACTCTGATGACATTTGATCTACACTCTCC
 TACTCTACTCTCTCTGATAAAAGTCATAATTCGGAGTTAATATTTTACGCTGATAT
 TGCTGTGATTGGGCTGTTGTGAATTTGTAACCTTTTAACTACCACTTGA**ACA**CTTAA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAAAAATGTAAGT
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAACTCATAAAAATTAAT
 TTAAGATGTCGGAAGAGGATACTTTGATTAAATAAAAACTCATGGATGTGTAAGAAATG
 CAAGATTAATTTAATAGTTTCAATTTATTTTATTTTGAAGAAATAGTGATGAAC
 AAAGATCTTTTTCTACTGATACCTGGTTGATATTTATTTGATGCAACAGTTTTTCTGAAAT
 GATATTTCAATTTGCATCAGAAAAATAAATCATCTGATGCTCAAAATAGCAAGGTAAA
 GGAGAGCAATTAACAACTTTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 274

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSGCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDfKNTIPMVTPPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLQLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQDVVSYRYFTAYTENGRYSLKVRAGH
 GANTARLKLRLPPLNRAAYIPGWVNGEIEANPPREIDEDTQTTLDEFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDNFDVGKVQRYIIRISASILDRLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCG
GGCAGGGGTGACAAACAGGTGTATCTTTTGTATCTCGTGTGGGTGCCTTCTTATTTCAAGGAAAG
ACGCCAAGGTAAATTTTGACCACAGGAGCAATGATGAGCCACCTCTCAACCTTCCCTTCTTGAACC
CCAGTATTGACAGGATTTACTAGAGAGTGTCAACTCAACAGCAAGCGGCTCCTTCGGCTTAACTT
GTGGTTGGAGGAGAAACCTTTGTGGGGTGCCTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGA
GGGTGGACAGAAAGAAAGGAGTCCCTCTTGTGTTGGCTGCACATCAGGAAGGCTGTGATGGG
AATGAAGGTGAAAATCTGGAGATTTCACTTCAGTTCAGTTCCTCTGCTGCAAGATCATCTTTAAAA
GTAGAGAAGCTGCTCTGTGTGGTGGTAACTCCAAGAGGCAGAACTCGTTCTAGAGAAGAAATGGATG
CAAGCAGCTCCGGGGGGCCCCAACGCATGCTTCTGTGGTCTAGCCCCAGGGAAGCCCTTCCGTGGGG
GCCCGGCTTTGAGGGATGCCACGGTCTTGGACGATGGCTGATTCCTGAAAGATGATGGTTCGCC
GGGCTGTCTTGGCTGGATTTCCGGGGTGTGCTTTGCTGTGCTCTCTGCTGTCTATCTCTGT
CCTGTACATCTTGGCTTGCACCCAAAAGTGCAGGAGCAGCTGGCACTGCCAGGGCCACAGC
CCACGGGGGAAGGGGGTCCACGGCCGTCTTCAAGAGTGGGAGGAGCAGCACCCAACTACGTGA
CGACCTTGAAGCGGCAGATCGCACAGCTCAAGGAGAGCTCGAGGAGAGGTGAGCAGCTCAGGAA
TGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAG
GCCGACCTCTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG
CCACAGAGTACGCAGCAGTGCCTTTGATAGCTTTACTCTACAGAAGGTGTACAGCTGGAGACTGG
CCTTACCCTGCCACCCGAGGAGAAGCCTGTGAGGAGGACAAGCGGGATGAGTTGGTGGAAAGCCATT
GAATCAGCCCTTGAGAGCCTGGAACAATCTGACAGAGAACAGGCCCAATCAGCGTCTCTACACGGCCCT
CTGATTTTCATGAAGGATCTACCCGAACAGAAAGGACAAGGGACATTTGATGAGCTCACCTTCAA
AGGGGACCAAAACAGCAGATTTCAACCGGCTCATCTTATTTCGACCACTCAGCCCACTCATGAAAGTG
AAAAATGAAGAGCTCAACATGGCCCAACACGCTTATCAATGTTATCTGTCCTCAGCAAAAGGGTGG
ACAAAGTTCGGCAGTTCATGCAGAAATTTGAGGAGATGTGCTATTGAGCAGGATGGGAGAGCTCAAT
CTAGTTGCTGCTTGGCTTACAGCAAGTGAATGAGCTGAATGAGCTGAGCTGACCAACTTCCAA
GCTGCCAATCTCAGGAACCTTACCTTACCTCCAGCTGAATGGAGAATTTCTCGGGGAAGGAGCTTG
ATGTTGGAGCCGCTCTGGAAGGGGAAGCAACGCTCCTCTCTTTTCTGTGATGTGGACATCTACTT
CACATCTGAATTCCTCAATAGCTGTAGGCTGAATACACAGCCAGGGAAGAAGTATTTTCCAGCTT
CTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGACGTCCCTCCCTTGGAAACAG
AGCTGGTCATAAAGAAGGAAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTGATATCG
GTCAGACTTCATCAATATAGTGGGTTTGTATCTGGACATCAAAGCTGGGGCGGAGGAGATGTGCCAC
CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGAGCCTGTGCGAGGACTCTTCCACC
TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGCATGCACTCCAA
GGCCATGAACGAGGCTCCACGGCCAGCTGGGCTGCTGTGTTGTTGACGACGAGATAGAGGCTCAC
CTTCGCAAAACAGAAACAGAGACAAGTAGCAAAAAAAGCATGAAGCTCCACAGAGAAGGATTTGTGGAGA
CAGTTTTTTCTCTTTTGCAATTTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAAGGACG
ACAAAGAAATTTGACATCTGGGTACAGATGCAAGAGCTCCGATTTCTCTCTGTGGCTTTTAC
AACAAGAAATCAAATCTCCGCTTTGGCTGCAAAAGTAAACCAGTTTGACCTGTGAAGTGTCTGACA
AAGGCAAGTGTGTTGAGATTATAAGCCTAATGGTGTGGAGTTTGCATGGTGTTTACAATACATCT
GAGACCTGTTGTTTTGTGTGCTCATGAAATATTCATGATTTAAGAGCAGTTTGTAAAAATCTACT
TAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGGCTCTAGTTTCTAGG
AATGTCAAAATATCAGAAGGCGAGGAGAGGATAGGCTTATTATGATACTAGTGAAGCATTAAGTA
AAATAAATGGACCAAGAAAGAAAGAAACATAAAATATCTGTCTATTTTCCCCAAGATTTAAACCA
AAATAATCTGCTTATCTTTTGGTTGTCTTTTAACTGTCTCCGTTTTTTTCTTTTAAAAAT
GCACTTTTTTTCCCTTGTGAGTTATAGCTGCTTATTTAAATACCACTTGAAGCCCTTACAAGAGA
GCACAAGTTGGCCTCAATTTTTATTTTTTAAAGAGATATCTTGAGATGCATATGAGAATTTCA
GTTCAAAGCATCAATGATGCCATATGCAAGGACATGCCAAATGCTGATCTGCGACCTGAAT
CTCAGGATTCAGCATGAGCAGAGTGTGTTGTCTATACAGAGTACAGTCTGCTCTCTGCTGAA
GACTTTTTTCAGACAGGACCACTGAACCTGGAGGAAAGAAATGACACTTTCTGCTTTACAGAA
AAGGAAACTCATTCACACTGGTGATATCGTGATGTACCTTAAAGTCAGAAACCATTTTCTCTCA
GAAGTAGGAGCGCTTTCTTACTGTTTAAATAAACCAAGATACCGTGTGAACCAACAACTCTCT
TTTCAAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATAAGAAAGAAATATATATATATATATAT
ATATATATATATTTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTGTCTACAT
TATTATCCACCTCAGGCGAGGTGGAAGTAACCTGAATTTATTTTAAATTAAGCAGTTCTACTCAATCA
CCAGATGCTCTTGAAAAATGCATTTTATACCACTTCAAACTATTTTTTAAAAATTAATACAGTTA
ACATAGAGTGGTTTTCTTCAATCATGTGAAATATATAGCCAGCACCATGCTAGCTAATTATCT
CTTGTGCTGCTGCTTCTGTTTGTCTCAGACTAACTCATTTGTTTAAAGAGCTTCAAGAAAGCTCAAG
TGTTGGTGTGTTAAAAAATGCATTTGATTGTTTGTACTGGTAGTTTATGAAATTAATAAAAAC
AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFL
HSQVDKAEVNAAGVKLATEYAAVPPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPI
MKVKNEKLNMAN TLIN VIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGAATGTTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCTGGACCCATCTGTGCCCCTCTG
 GATTATTATATTGGTGTGATATTTGCATCATCATAGTTGCAATTGCCTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAGAACAAAGAACCCTCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCTGGACATGAAGG
 GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTTCTTTGTAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
 TCAAAATATTCTAAATATTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTGTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAACTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGGAAAT
 TTATCTGTATTACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGGTTTCCCTC**CATGT**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGAAATTTATACCTCCCGGGTCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAATGCACCTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGTCTTATTTAATTCAGA
 GTGTAATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCCTTAA
 GACACTACTTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCTTTTACGTATTCTTTTACGAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTTTTCTTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAACAGTAAATCCTAAATTCAAAGTGTAAATGACATTTTATTTTTATGTCTC
 TCCTTAACATATGAGACACATCTTGTCTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
 TTTGTCTG

FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMSGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVI GEIRLSVVHTVRFSEIHFLALALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKKVSVYLETD

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACCTATTCATGCTTCCTGTGATTTT
ATCCAACCTACTTACCTTGCCCTACGATATCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAA

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTTAT
 TAASTTARKDIPVLPKWVGDLPNGRVCP

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTGCTGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTGGGTGAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTGTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
 GCAAATCCATAAAGAACCAGAGGGTCTGGGCCCCGCCACAGAGTCATCTGCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTGTGCCAG**TAA**AACACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATTAAACTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCGTGTAATCCAGCACTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
 GCAGGAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 285

GTCAATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCAGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCCTGAATCTGCCTGGATGGAAC TGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCATGCCTACACACCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTQLGQALNGVYRTTEGRLTK
ARNSLGLYGRRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGATGGACTTGTAAATTTGCAT
 CCTGGTGATCACCTTACTCTGGACCAGACCACCAGCCACACATCCAGATTAAGAGCCAGGA
 AGCAGAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCAAGAAGATGTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAATCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGTACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGAGCAGCAAGAGATACATATCGAGTTTACCATCCC
 TAAATAGGTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTGTCTCATCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTTGAAGTTTCCAGCCGAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTCCCACCATTCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAAGCTGAAAACGAATTTAAAGAATGCTATCTTGGAAAATGATACGCTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTGTGTTTAACTAGATTGTACAAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTCATTGTCTCA
 ATAATAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSPLPGVNDFWLGINDMVTGEKFDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTTCCCCGCGCGC
CCCAGACCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGTGGGG
GCCCTGACAGTGTTTGGCTTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACC CGCAGGGCTGAAAACCCCGCCGGGGAGGACCGTCCATCCCCTCCCCCGGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

[illegible][illegible][illegible]

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAT
 CCTTGGCCTCCGCAGCCGATCACAATGAAGGTGGTGCCAAAGTCTCCTGCTCCTCGTCCCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGCTGAGGAAGAGAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACTTCGGATTACGCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCAACCAAG
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCCTCTCCCGAACCTGGAACT
 GGGCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTAATTAACAAGAGACTCGGGGGAAAATTTCCAAAAT
 GTTTGATGAGATTAATCTGAAACCAATTAATTTCTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCATTGACCCCTGTCTTCACCGAAGTCGACACTTTCCACTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCCTCCACCTTTGACAAAGAA
 TTTTCGTTGTCTATGTCTCAAACCTGCCCCACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCCATGCCTCCTGTCTCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATTAATTTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTCTTTGTTCTTAAGTGTAGGGTGTCTC
 AAATAAATACAGTAGTCCCACTTATCTGAGGGGATACATTCAAAGACCCCAAGCAGATGC
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTCATTTAATGTTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAGCAAAACCATGGATGAAGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAA

MKVVPSSLLSVLLAQWLVPLGLAPSPQSPETAPQNQTSRVVQAPREEEEDQEASEEKAGE
 EEKAWLMASRQQLAKETSNFGFSLLRKISMRHDGNMVFSPFGMSLAMTGLMLGATGPTETQI
 KRGLHLQALKPKPKPLPSLFKGLRETLNRNLEGLSGGSFAFIHKDFDVKETFFNLISKRYF
 DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKILVDYIILFKGKWLTPFDP
 VFTEVDTHFLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
 ALEDYLTDDLVEWLRNMKTRNMVEVFFPKFLDQKYEMHELLRQMGIRRI FSPFADLSLSA
 TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPIKVDRPFHFMIEYETSGMLLF
 LGRVNSPTLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGAC**ATGAG**
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGGCCGTGTCTGAGTCCC
GAGCCCAGCCATGACAGCCTGTACCACCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCA**GTAG**GGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Carotenoids*
 4. *Phycocyanin*
 5. *Peridinin*
 6. *Algae*
 7. *Phaeophytin*
 8. *Phaeopigments*
 9. *Phaeoerythrin*
 10. *Phaeo-*a**
 11. *Phaeo-*b**
 12. *Phaeo-*c**
 13. *Phaeo-*d**
 14. *Phaeo-*e**
 15. *Phaeo-*f**
 16. *Phaeo-*g**
 17. *Phaeo-*h**
 18. *Phaeo-*i**
 19. *Phaeo-*j**
 20. *Phaeo-*k**
 21. *Phaeo-*l**
 22. *Phaeo-*m**
 23. *Phaeo-*n**
 24. *Phaeo-*o**
 25. *Phaeo-*p**
 26. *Phaeo-*q**
 27. *Phaeo-*r**
 28. *Phaeo-*s**
 29. *Phaeo-*t**
 30. *Phaeo-*u**
 31. *Phaeo-*v**
 32. *Phaeo-*w**
 33. *Phaeo-*x**
 34. *Phaeo-*y**
 35. *Phaeo-*z**
 36. *Phaeo-*aa**
 37. *Phaeo-*ab**
 38. *Phaeo-*ac**
 39. *Phaeo-*ad**
 40. *Phaeo-*ae**
 41. *Phaeo-*af**
 42. *Phaeo-*ag**
 43. *Phaeo-*ah**
 44. *Phaeo-*ai**
 45. *Phaeo-*aj**
 46. *Phaeo-*ak**
 47. *Phaeo-*al**
 48. *Phaeo-*am**
 49. *Phaeo-*an**
 50. *Phaeo-*ao**
 51. *Phaeo-*ap**
 52. *Phaeo-*aq**
 53. *Phaeo-*ar**
 54. *Phaeo-*as**
 55. *Phaeo-*at**
 56. *Phaeo-*au**
 57. *Phaeo-*av**
 58. *Phaeo-*aw**
 59. *Phaeo-*ax**
 60. *Phaeo-*ay**
 61. *Phaeo-*az**
 62. *Phaeo-*ba**
 63. *Phaeo-*bb**
 64. *Phaeo-*bc**
 65. *Phaeo-*bd**
 66. *Phaeo-*be**
 67. *Phaeo-*bf**
 68. *Phaeo-*bg**
 69. *Phaeo-*bh**
 70. *Phaeo-*bi**
 71. *Phaeo-*bj**
 72. *Phaeo-*bk**
 73. *Phaeo-*bl**
 74. *Phaeo-*bm**
 75. *Phaeo-*bn**
 76. *Phaeo-*bo**
 77. *Phaeo-*bp**
 78. *Phaeo-*bq**
 79. *Phaeo-*br**
 80. *Phaeo-*bs**
 81. *Phaeo-*bt**
 82. *Phaeo-*bu**
 83. *Phaeo-*bv**
 84. *Phaeo-*bw**
 85. *Phaeo-*bx**
 86. *Phaeo-*by**
 87. *Phaeo-*bz**
 88. *Phaeo-*ca**
 89. *Phaeo-*cb**
 90. *Phaeo-*cc**
 91. *Phaeo-*cd**
 92. *Phaeo-*ce**
 93. *Phaeo-*cf**
 94. *Phaeo-*cg**
 95. *Phaeo-*ch**
 96. *Phaeo-*ci**
 97. *Phaeo-*cj**
 98. *Phaeo-*ck**
 99. *Phaeo-*cl**
 100. *Phaeo-*cm**
 101. *Phaeo-*cn**
 102. *Phaeo-*co**
 103. *Phaeo-*cp**
 104. *Phaeo-*cq**
 105. *Phaeo-*cr**
 106. *Phaeo-*cs**
 107. *Phaeo-*ct**
 108. *Phaeo-*cu**
 109. *Phaeo-*cv**
 110. *Phaeo-*cw**
 111. *Phaeo-*cx**
 112. *Phaeo-*cy**
 113. *Phaeo-*cz**
 114. *Phaeo-*da**
 115. *Phaeo-*db**
 116. *Phaeo-*dc**
 117. *Phaeo-*dd**
 118. *Phaeo-*de**
 119. *Phaeo-*df**
 120. *Phaeo-*dg**
 121. *Phaeo-*dh**
 122. *Phaeo-*di**
 123. *Phaeo-*dj**
 124. *Phaeo-*dk**
 125. *Phaeo-*dl**
 126. *Phaeo-*dm**
 127. *Phaeo-*dn**
 128. *Phaeo-*do**
 129. *Phaeo-*dp**
 130. *Phaeo-*dq**
 131. *Phaeo-*dr**
 132. *Phaeo-*ds**
 133. *Phaeo-*dt**
 134. *Phaeo-*du**
 135. *Phaeo-*dv**
 136. *Phaeo-*dw**
 137. *Phaeo-*dx**
 138. *Phaeo-*dy**
 139. *Phaeo-*dz**
 140. *Phaeo-*ea**
 141. *Phaeo-*eb**
 142. *Phaeo-*ec**
 143. *Phaeo-*ed**
 144. *Phaeo-*ee**
 145. *Phaeo-*ef**
 146. *Phaeo-*eg**
 147. *Phaeo-*eh**
 148. *Phaeo-*ei**
 149. *Phaeo-*ej**
 150. *Phaeo-*ek**
 151. *Phaeo-*el**
 152. *Phaeo-*em**
 153. *Phaeo-*en**
 154. *Phaeo-*eo**
 155. *Phaeo-*ep**
 156. *Phaeo-*eq**
 157. *Phaeo-*er**
 158. *Phaeo-*es**
 159. *Phaeo-*et**
 160. *Phaeo-*eu**
 161. *Phaeo-*ev**
 162. *Phaeo-*ew**
 163. *Phaeo-*ex**
 164. *Phaeo-*ey**
 165. *Phaeo-*ez**
 166. *Phaeo-*fa**
 167. *Phaeo-*fb**
 168. *Phaeo-*fc**
 169. *Phaeo-*fd**
 170. *Phaeo-*fe**

MRRLLLVTSLVVLLWEAGAVPAKVP IKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEKEPRQGGRGILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGGAGGAGTGAAGGAGCTCTCTG
TACCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGGCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGAATTCACTGCGGGATT
TGTTCACTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTTGTCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCAGCAGTGTGGAGATTTTCTGGTTTGTATTGGAGTGGATATGGAATCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL
FYR

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FIGURE 297

GCGGAGCCGGCGCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGACTCGGCGCGCGAGGTGCTTGGGCGG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAATATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTCT
 CTTTTTGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCCTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCACTACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTCACAGCACTCAGGATTTGGGTATCTTTTGT
 AGCTCACATAAAGAAGTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACATAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGLTQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
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FIGURE 299

CAGCCGGGTCCTCCAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGCATGGCGCACCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCTGGCGCTTTCGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAATTTGAGGATGTCAGATGTAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCTCT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTTGGGGATCACCAGCCTTT
 TGCAATGCACAGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAAACCTTGTGATTTTACCAACT
 GTTGTGGAAGATTCAAAACCTGGAAGCAAAAACCTTGCTTGATTTTTTTTCTTGTAAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTTTGTTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGATGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
 ACTTTTGCAGTACTGTATTATCTGGGTATCTGCTGTGCTGCACCTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTTATTGGATAACTGGCTTTTT
 TCTTCTATGTCTCTTTGGAATGTAACAATAAAAAATAATTTTGAACATCAA

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FIGURE 300

MATLWGGLRLGSLLSLCLALSLLLLLAQLSDAAKNFEDVRCKCICPPYKENS_{GH}IYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLLYMVYLT
LVEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLRASRSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVL

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FIGURE 301

GCACCTGCGACCAACCGTGAGCAGTCAATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCGCCGACACCTGAAGGAAAATTGGGCGGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAACCTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCACTTTCACATAAGAAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAATTCACAATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLKAFLSRGKRQEPPPTPEGKLGFRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPIYGFGLYILYILFKVSRILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCTCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGC**CATG**TTTTGCCCCTGAAACTCATCTGCTGCCAGTGTAC
 TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTGAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGACATCTTATGC
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGATTGATTGAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTCCATCATG
 CTTCAAGAGTGAAGGAGTCAAGTGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGAAGAGCCTCGAAGACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCTTGCATTTTGAAAGATGTGAAGGGGAGAAACACATTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGAGA**AAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCTGTGTGTGCTGGGCCACTCTACCAGTGATTTGAGACTCCCGCTCTC
 CCAGCTGTCCTCTGTCTCATTGTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGAAGTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGGCTCAAACCCCGTT
 GGATCAGACCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLIILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEVLYYYSNLSVPIGRFQNRVHLMGDI LCNDGSLLLQDVQEADQGT YICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGG LIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGMPKTQQAF

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FIGURE 305

CTATGAAGAAGCTTCTCTGAAAAACAATAAGCAAAGGAAAAACAATGTGTCCCATCTCACATG
GTTTCTACCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGC AAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGGGGCTGGTGGCTCTGGGGATTTGGTCTGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAAGCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
TAAGCAGTACTGCAC TGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

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FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCCGG
CCCGGGGCTGTGGCTGCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGCGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTCCGGAGAA
GCCCCGGCAAACGCGAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTCCCGGGTCAAACCTCTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTGTTGAAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGCCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC
G**TAG**CCAGTGAGGGGCAAAAGAAGGGCTCTGTAAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTACATTACCAAACAAACAGG
CAGAGTTCACCTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVFSRVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGYLYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCTGTAGATTAC
 AAGAGTGGATTGTCAGGAGTGTGCCCCAAAATACAGTGAAAGGTGCCTGAAGATATTTAA
 ACCACGCTCTTGAAATTTAGTGGGCTCTTGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTCCG
 CGCAGCGGCGCGTGTGTCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCAGCCAGAGGATACCAAGTCTCCTCACCCACTTCAACCTGATCCCT
 GTGGGCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGGAGGCTCCCTTCCAGTCCCCCTGCCCTTGAAGTGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKLCQQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGCCATCGCTAGCGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCGCTGTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTGAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWD RPSASRRSSPSK NRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQ MHPD GALT DGT KDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQ QESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTFSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAAT
 GAAGGATGCGAGACGCGACTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AAATAAACAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCC
 CTCCCCACCCCAAAAAAGGATGATTGAAATGAAGAACGAGGATTCAAGAAAGAAAAAGTATTGTTCATT
 TTCTCTATAAAGGAGAAAGTGAGCCAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAAGCTGGTGGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGC
 AAAGAAATTTGAGAGAGAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAAATGACGGATAAATGCGATTGGATTTTTCTTCATCAACCTCCTTT
 TTTTTAAATTTTTATTCTTTTGGGATCAAGATCATGCGTTTTCTTGTCTTAACCACTGGATTTCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAGGACCAACACCAGATAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGTTTAAACAGGGCCCTATTGACCCCT
 GCTTGTGTGCTGCTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGGCGGCTCAGACCTGCCCTTCTGTGT
 GCTCTGCGACCAACAGTTGACGAAGTGATTGTGTTGCGAAAAACCTGCTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCGATGAGAACCAATCCAGATCATCAAAATGAACAGCTTCAAGCACTTGA
 GCACTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTGTATACTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAAATCCTTCTTT
 CGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCACAT
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCACAGGTTTGATGCACTTCAAAAACT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGCACTATGAGCGGATACAT
 GTACATCACAAACCTTGGAACTGTAAGTGTGACATACTGCGCTCAGCTGGTGGATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCGGTGTAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGCGGCCCTCCACATCCCTGACATCTGTATCTTGATTAATCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAGTGGGATGAGCTGTGCTCAGTGATGGTACAGTTAAATTTACAAAGTGTAACTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAGTAATCCGTTGGGAATCACTACTGCTTCAGCCACCCTGAATGTTACTGCA
 GCAACCACTACTCCTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCACG
 GACCACAGATAAACAATGTGGTCCCACTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGTGCAGAGAGAAACCTTCAACATCCAGTGACTGATGATTAACAAAGTGTAACTGTGCAAGATA
 GATGAGGTGATGAAGACTACCAAAATCATCATTGGGTGTTTTTGGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGGAGCTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCATGGAAGCCACCTGCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAAATCATACAATCTCCCTTCAACACACACACAGTTAAACAAATAAATCAATACA
 CAGTTTCAGTCATGACCGTTATTGATCCGAATGAACCTTAAGACAAATGTACAAGAGACTCAAAATCTAAACAA
 TTTACAGAGTTACAAAAAACAAACATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTACAAAAAACAAAAAGAAAGAAATTTATTTATTAATAAATCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKM T L H P Q Q I M I G P R F N R A L F D P L L V V L L A L Q L L V V A G L V R A Q T C P S V C S C S N Q F S K V I C
 V R K N L R E V P D G I S T N T R L L N L H E N Q I Q I I K V N S F K H L R H L E I L Q L S R N H I R T I E I G A F N G L A
 N L N T L E L F D N R L T T I P N G A F V Y L S K L K E L W L R N N P I E S I P S Y A F N R I P S L R R L D L G E L K R L S
 Y I S E G A F E G L S N L R Y I N L A M C N L R E I P N L T P L I K L D E L D L S G N H L S A I R P G S F Q G L M H L Q K L
 W M I Q S Q I Q V I E R N A F D N L Q S L V E I N L A H N N L T L L P H D L F T P L H H L E R I H L H H N P W N C N C D I L
 W L S W W I K D M A P S N T A C C A R C N T P P N L K G R Y I G E L D Q N Y F T C Y A P V I V E P P A D L N V T E G M A A E
 L K C R A S T S L T S V S W I T P N G T V M T H G A Y K V R I A V L S D G T L N F T N V T V Q D T G M Y T C M V S N S V G N
 T T A S A T L N V T A A T T P F S Y F S T V T V E T M E P S Q D E A R T T D N N V G P T P V V D W E T T N V T T S L T P Q
 S T R S T E K T F T I P V T D I N S G I P G I D E V M K T T K I I I G C F V A I T L M A A V M L V I F Y K M R K Q H H R Q N
 H H A P T R T V E I I N V D D E I T G D T P M E S H L P M P A I E H E H L N H Y N S Y K S P F N H T T V N T I N S I H S S
 V H E P L L I R M N S K D N V Q E T Q I

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

CGCGCCGGAGGCCATCTGCCCCAGGGGCACGGGGCGCGGGGCGCGGCTCCGCGCCGGCACAT
GGCTTGCAGCCACCTCGGCGCCACCCGAGGGCGCGCGCCAGCTCGCCCGAGGTCGCTCGGA
GGCGCCGGCGCCGCCGAGGCCAGCAGCAACTGACGGGGAAGCGCCGCTCGGGGATC
GGC**ATGT**CCCTCTCCTCTCTCTCTTGTCTACTATGTGGAACCTTGGGGACATCA
CACCTGAGATCAAGAGAGTGGCAGGAGAAAGTTCCTTTGCCCTGCCACCATCACTGGGG
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAAGGAACAAAAA
GTGGTGATCACTTACTCCAGTCGTCTATGTCTACAATACTTGACTGAGGAACAGAAAGGCC
AGTGCCCTTTGCTTTCCAATTCTGCGACGAGAGTGCCTCTTGAGATTGAACCTCTGAAG
CAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTAGGGCGCTACGTGTGGAGCCAT
GTCACTTTAAAAGTCTTAGTGAGACCATCAAGCGCAAGTGTGAGTTGGAAGAGAGCTGAC
AAGAAGAAAGTGAAGTCACTTTGCACTGTGAGTATCCTCTGGCACAGAGCCATTGTGTATT
ACTGGCAGCGAACTCCAGAGAAAGAGGGAGAGTGAAGCTCTGCCCTCCAAATCTAGGATT
GACTACAAACCCCTGGACGAGTCTGTCTGCAGAAATTTACCATTCTCTACTCTGGACTGTA
CCAGTGCACAGCAGGCCAACGAGCTGGGAAGGAAAGCTGTGTGGTGGGAGTAACCTGTACAGT
ATGTACAAGCATCTCGGATCTGTGTACCGACAGCTGACAGCATAGTGCGCTGGAGCCCTGCTG
ATTTTCTCTTGTGTGTGCTGCTAATCCGGAAGGAAGACAAAGAAAGTATTGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTCTCTCAGGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCCACCTCGCTCCACAGAAAT
AGTGCCTCAGCAGCCAGCGGACATGTCTCAACTCAGCAGCACCCAGCCAGGCTGGCCAC
CCAGGCATACAGCGCTAGTGGGGCCAGAGGTGTGAGAGGTTCTGAACCAAAAGAAAGTCCACCAT
CTAATCTGACAGCCAGAAACCAAGCCAGCATGATCCCCAGCCAGAGCAGGCTTCCAA
ACCGTCT**TGA**ATTACAATGGACTTGACTCCCAAGCTTCTCAGAGTAGCGGTCTTTGGACTC
TTCTCTGTCATTTGAGCTCAAGTCAACAGCCACACCAACAGATGAGAGGTCTACTTAAGTAGCA
GTGACGATTGCAAGCAACGATTTCAGTAGCAATTTCTCTATACATACCAACAAAGCAAA
AGGATGTAAGCTGATTTCATCTGTAAAAGGCATCTTATTGTGCTTTAGACAGAGTAGAAGG
AAAGCGAGGAGTCCAAATCTATTGTTGACCAAGGAGCTGTGGTGAGAAGTTGGGGAAGGTG
AGGTGAATATACCTAAATCTTTAATGTGGGATATTGTTGATCAGTGCTTTGATTACAAT
TTCAAGAGGAAATTTGGGATGCTGTTGTAATTTTCTATGCAATTTCTGCAACTTATTGGATT
ATTAGTTATTACAGAGTCAAGCAGAACCCACAGCGTTATTACACCTTCTACACATGTAC
TGAGCTAACCACTTCTAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCTAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCATCTATCACTAATCTCATATTGTGATTGAGCCCAAATTAAC
TATGAAGGAGACAAAAATTTGTGAAAGAGGATTGTGAAGAGTTTCCATCTCTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGGATTTCCCTCAAT
CAGATGCTCTAAGGACTTTCTGCTAGATATTCTGGAAGGAGAAATACAAATGTCAATT
TATCAACGTCCTTAGAAGAAATCTCTAGAGAAAAAGGGATCTAGGAATGCTGAAGATTA
CCCAACATACCAATTATAGTCTCTCTTTCTGAGAAATGTGAACACGAATGTGAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
TGGTGCACCGGCCTGTAGGAAATCCAGCAGGTGTGAGGTGCACTGAGCCGAGATTATGCC
ATTGCACTCCAGCTGGGTGACAGAGCGGAGCTCCGCTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
 VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
 ILKVLVRPSKPKCELEGELETEGSDLTLCCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
 YNHPGRVLLQNLMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
 FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPPSSSSSGSRSSRSGSSSTRSTANS
 ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

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FIGURE 317

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHVLVLKPSGARCYPVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVSGDQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
 CTC AAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCAGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTCTACTTGAAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTGTTCCCTGTGTCAATTC
 AACAGTCTCCCTTCCCTATGCTGTTCACTGGACACTTCACGCCCTTGCCATGGGTCCCATT
 TTGGCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATGTGCCCATGCTTCTTTACCCCTCACAATCCTGCCACAGTGTGGGCGAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACCTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGGCCCTCCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTC CAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRRLQSLWTLARPFPCPLLATASQMOMVVLPCIGFTLLLSQVSGAQGGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAAGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
CACTGGCTGGCTCAGGCTGTCTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTIIILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
 GGTTCCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACC**ATG**TTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTTCGAC
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
 TCAGTATCACCTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCGTACTCCAGTTCCCTGTCCCGAGGAACGAGATCCCCCTAATTCACCTCAACACC
 CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
 GCTGAAGCCCCGGGCGCGGATGACCCCGGCCCGGCCCTCCTGTTACAGGAGCTCCCAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGTGGTCAGGGCGCGTTCGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATC**TAG**GGTCTG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY
DVIHSPQYHFLVSLGRAKRAFLPGMNPYPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGGATG
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACATGCGATGACACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCCGGGCCACGCCGCTCTGGAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTCACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCGTCAT
 GGTCCCCGGGATCTGATGTCACCTCTCTCGTGAAGCCCTGGTGACTGTCAAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACACTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTG
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGACAGTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCCT
 CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACGTGAGTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGTGAGTG
 TGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGCTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTCACTGTTCAGAGGTGTCCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCCTGCA
 TTAAATTCACTCAGTGTGCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSEA
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTTKTSPNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAI FDTLCTDDSEEAKTLTMDILT LAHTSTEAKGLSSESSASSDGHPV
 ITPSRASESSASSDGHPVITPSRASESSASSDGHPVITPSWSPGSDVTL LAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALSVETPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGFPTSRD
 PLPSVPPTTTNSSRGNTSLAKITTS AKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCAGCTGGATGGCAGAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGTCAGCCTTCTTAAAGCAAATTAAGACCAGAGGGAGGATTAT
 CTTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGCTTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATTT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTATGACATCCAGTCATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAAGACTGCATTAAATCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCTGAAATGTGAGTGCAGTCCCAGCTAGCGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCTCCACAGACCCTCATTTTCTACAGTTTTTACACGGGCTGCGGTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATAACCGTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAGGTT
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTTCCAGAAATCACTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGGGTAGAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGGCCAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCTTCTGCTTTTCTTTTTTTTTTGGAGACAGAGTCTTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGACAGGGGTTCCACCATTGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCTCGGCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAAATTAGTAATTTTGGGTAATCTGCTCTAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTTCATTCACATTCTGGTCCAGATAAAATCAAC
 TGTTTATCAATTTCTAATGGATTTGCTTTCTTTTATATGGATTCTTTTAAACCTTATT
 CCAGATGTAGTCTCTCAATTAATATTGAATAAACTTTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMI FDRKTRARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLHGGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIHLHPENVSAIPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKATASWEGREASPGSSSQGSV
PENQYGLPFEEKWLLIGSLLFGVLFVLVIGLVLLGRILSESIRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGCGCCAGAA**ATG**CGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGAACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCCGTCTTTCCAGGACCTGCTGTCTCCCTCCCCTTCTCCCAC
 CTTCCAGCTCTGGCTACAACACGCTCGAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGGCTCTACCCGGCAGCCACACAGCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCATGCGAG
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCACAG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTCTGAGCCTTCTGTACGC
 CGCAGGCCCTGATCGCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCTTGACTCGGAGGAGAAAGGCC
 CCTTCCAGGCCCTCAGGAGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCG**TAGGGC**CAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCCTCAGAG
 TCCAGCTTGCCCGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTGTCATGTTTCCA
 GCCTGACCTAGAAGCGTTTTGTAGCCCTGGAGCCAGAGCGGTGGCCTTGCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 TCTATGCCACGTGTCCGACCCTGCCTTCCCTCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTCAGGAAGCCT
 GTGAAAACGCTGATTCTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGAG
 GACTCTGAATTCTAACAATGCCAGTGAAGTCTGCGCACTTGAGTTTGAAGGCCAGTGGGCGTG
 ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTCCACCTGCCC
 CAATAGATCTGCTCTGTCTGCGACACACAGATCCAGCTGGGGACTCCCTGAGGCTGCTAAG
 TCCAGGCTTGGTCAGCTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTGTGCCCTCCCTGNNCATGCCTTCTGGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTGTCTGGAAGGGTTACTTGCCCTATGGGTCTTGGTGGCTAGAGA
 GAAAAGTAGAAAAACAGAGTGCACTAGGTGTCTAACAACAGAGGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGGGGGGTGGTGGTAAAGTA
 GCACAACCTACTATTTTTTTCTTTTTTCCATTATTTATGTTTTTAAAGACAGAATCTCGTGCT
 GCTGGCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCGCCCTCTGGGTTCAAGTGATT
 CTCTCTGCTCAGCTCCCGAGTAGCTGGGATTACAGGCACGACCACCACCTGGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAAATGAGCCTCCTGCTCAGTCTCCCAAAATGGCCGGATTACAGGATGAGCCTGTG
 TCTGGCCCTATTTCTTTTAAAAAGTGAATTAAGAGTTGTTTCAATGCAAACTTGGAAAG
 ATGGAGGAGTAAAGAAAGAAAGAAAGAAAAAATGTCACCCATAGTCTTCCAGAGACTCAT
 TATTTCTGTTTTGTTGACTTCTTCCACTCTTTTCTTCTTACATAAATTTGCCGGTGTCTT
 TTTACAGAGCAATTTATCTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTTCCAGCACTCTCTGTGTTTTACAGACCTTTTATAAATAAATGTTCTACA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGP EEISGFEGD TVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLTLQDAGEYWCGVEKRGPD ELLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGTGA EAPPLPG
TSQYGHERTSQYTGTSFHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFC SHLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
VISMPPLHTSE EELGF SKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128